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OM nucleic - nucleic search, using sw model

Run on: July 30, 2004, 19:06:11 ; Search time 380 Seconds
(without alignments)
268.307 Million cell updates/sec

Title: US-09-831-272-7
Perfect score: 24
Sequence: 1 cagccaccaagagaccagat 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1808:*
2: geneseqn1908:*
3: geneseqn2000:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	24	100.0	41	3	AAA27970
2	19.8	82.5	431	7	ABx62031
3	19.8	82.5	2868	6	ABZ12691
4	19.8	82.5	2868	7	ADA68110
5	19	79.2	141	3	AAA52645
6	19	79.2	3062	6	ABK84368
7	19	79.2	3062	6	ABN96885
8	19	79.2	3062	7	ABD18955
9	19	79.2	3205	7	ABZ68460
10	19	79.2	3205	7	ABZ68462
11	19	79.2	3205	9	ADCI0127
12	19	79.2	3692	2	AAV00090
13	19	79.2	3692	2	AAV00160
14	19	79.2	3692	2	AAV01027
15	19	79.2	3692	9	ADBS6419
16	19	79.2	3692	9	ADBS5000
17	19	79.2	18772	4	ADBI6561
18	19	79.2	18772	6	ABSG64151
19	19	79.2	18772	9	AAAD60460
20	18.8	78.3	1866	4	ABL28935
21	18.2	75.8	41	6	ABZ43339
22	18.2	75.8	41	6	ABZ46679
23	18.2	75.8	2877	7	ADA71007

24	18.2	75.8	3187	4	ABU05460	Abi05460 Drosophila
25	18.2	75.8	5159	9	ADD44763	Add44763 Human gen
26	18.2	75.8	6353	4	ABU07173	Abi07173 Drosophila
27	18.2	75.8	8429	4	ABU07172	Abi07172 Drosophila
28	18.2	75.8	110000	3	AAE22303-4	Continuation (5 of
29	17.8	74.2	436	8	ACD06211	AcD06211 Human CDN
30	17.8	74.2	446	8	ACD06210	AcD06210 Human CDN
31	17.8	74.2	529	8	ACD06213	AcD06213 Human CDN
32	17.8	74.2	110000	6	ABA90521_16	Continuation (17 of
33	17.6	73.3	693	7	ACA31733	AcA31733 Frokaryot
34	17.6	73.3	746	4	AAU01196	AAU01196 Human rep
35	17.6	73.3	746	4	ABU96655	AbU96655 Human tes
36	17.6	73.3	1398	5	AA882726	AA882726 DNA encod
37	17.6	73.3	1657	4	ABU18193	AbU18193 Drosophila
38	17.6	73.3	3117	5	AA890916	AA890916 DNA encod
39	17.6	73.3	5304	7	ADA98924	Ada98924 Human sec
40	17.6	73.3	5304	7	ADA44528	Ada44528 Human sec
41	17.6	73.3	5304	9	ADC20962	AdC20962 Human sec
42	17.6	73.3	7055	4	ABU18192	AbU18192 Drosophila
43	17.6	73.3	79467	8	ADA02717	Ada02717 Mouse Nfa
44	17.6	73.3	79467	9	ADB72455	AdB72455 Mouse Nfa
45	17.6	73.3	154465	6	ADD28763	AdD28763 Human AKA

ALIGNMENTS

RESULT 1	AAA27970 standard; DNA; 24 BP.
AAA27970	
15-AUG-2000 (first entry)	
Box S elicitor-responsive cis-element nucleotide sequence.	
Box S, elicitor-responsive cis-element; parsley; PPI promoter;	
chimeric promoter; pathogen infection; transgenic plant; resistance;	
herbicide; local response; genetic engineering; disease resistant crop;	
eli 7; ss.	
Petroselinum crispum.	
WO200029592-A2.	
25-MAY-2000.	
12-NOV-1999; 99WO-EP008710.	
12-NOV-1998; 98EP-00121160.	
27-NOV-1999; 99EP-00116981.	
(PLAC) MAX PLANCK GES FOERDERUNG.	
Kirsch C, Logemann R, Hahlbrock K, Rushton P, Somschich I;	
WPI; 2000-387804/33.	
Chimeric promoters mediating gene expression in plants upon pathogen	
infection, useful for transgenic plant production comprises at least one	
cis-acting element to direct elicitor-specific expression.	
Claim 1; Page 29; 73pp; English.	
This sequence represents Box S, an elicitor-responsive cis-element	
necessary for the expression of the Parsley eli 7 genes. The present	
invention relates to chimeric promoters capable of mediating local gene	
expression in plants upon pathogen infection. The chimeric promoters	
comprise at least one cis-element (see AAA27964-A27979) capable of	
directing elicitor-specific expression, and a minimal promoter. The	
chimeric promoters are useful for producing a transgenic plant which has	
attained resistance or improved resistance against a pathogen. The cis-	

CC acting element, chimeric promoter, recombinant gene encoding the chimeric
CC promoter, vector comprising the chimeric promoter and a compound capable
CC of activating the chimeric promoter are useful for producing pathogen
CC resistant plants, and for identifying and/or producing compounds capable
CC of conferring induced resistance to a pathogen in a plant. A compound
CC which specifically activates or inhibits genes activated in a plant when
CC attacked by a pathogen is also useful as a plant protective agent or a
CC herbicide. The chimeric promoter provides rapid and local response to
CC pathogen attack but shows negligible activity in uninfected parts of the
CC plants and therefore is most suitable for the engineering of disease
CC resistant crops

CC SQ Sequence 24 BP; 10 A; 8 C; 5 G; 1 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 24; DB 3; Length 24;
CC Best Local Similarity 100.0%; Pred. No. 0.79;
CC Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGCCAGAAAT 24
DB 1 CAGCCACCAAGAGAGAGCCAGAAAT 24

RESULT 2
ID ABX62031 standard; DNA; 431 BP.

AC ABX62031;
XX
DT 25-FEB-2003 (first entry)

DE Arabidopsis thaliana expressed sequence related polynucleotide #146.
XX
XX Transgenic plant; plant; genetically modified cell; environmental stress;
KW ribozyme creation; disease resistance; stress tolerance;
KW fungicide screening; insecticide screening; gene; ds.
XX
OS Arabidopsis thaliana.
XX
PM US2002040490-A1.
XX
PD 04-APR-2002.
XX
PF 26-JAN-2001; 2001US-00770423.
XX
PR 27-JAN-2000; 2000US-0178512P.
XX

PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAM/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WORS/) WORSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRICK/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALJE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX

PI Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX
XX WPI; 2003-110411/10.

XX
PT Novel Arabidopsis thaliana nucleic acid useful for identifying homologous
PT or related genes, and to create genetically modified and transgenic
PT organisms, such as plant cells and plants.

XX
PS Claim 1; SEQ ID NO 146; 431p; English.

XX
CC The invention describes an Arabidopsis thaliana nucleic acid (I). The
CC polypeptide (II) encoded by (I), transgenic plant (III) or genetically
CC modified cell (IV) are useful for screening a candidate agent for its
CC biological effect, by combining the candidate agent with (II), (III) or
CC (IV), and determining the effect of the candidate agent on (II), (III) or
CC (IV). (I) is useful for identifying homologous or related genes, for
CC producing compositions that modulate the expression or function of its
CC encoded protein, for mapping functional regions of the protein, in
CC diagnosis, for studying associated physiological pathways, for genetic
CC manipulation of cells, preferably plant cells, in screening assays of
CC various plant strains to determine the strains that are capable of
CC withstanding a particular disease or environmental stress, for enhancing
CC or inhibiting production of biosynthetic product in a plant, for
CC producing polypeptides, as probes for the detection of mRNA in biological
CC samples, to generate additional copies of (I), to generate ribozymes or
CC oligonucleotides, as single stranded DNA probes or as triple-strand
CC forming oligonucleotides, and to create genetically modified and
CC transgenic organisms, such as plant cells and plants. (II) or (III) is
CC useful for introducing or improving disease resistance and stress
CC tolerance in plants, screening biological active agents, e.g.,
CC fungicides, insecticides, etc., and for elucidating biochemical pathways.
CC (III) is useful as crops for their enhanced disease resistance, enhanced
CC traits of interest, for screening programs, as crops which exhibit
CC enhanced tolerance to environmental stress, or to produce a factor. This
CC sequence represents a nucleic acid that may correspond to naturally
CC occurring Arabidopsis thaliana expressed sequences. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?docID=99909770423
XX

CC SQ Sequence 431 BP; 124 A; 77 C; 103 G; 127 T; 0 U; 0 Other;

CC Query Match 82.5%; Score 19.8; DB 7; Length 431;
CC Best Local Similarity 91.3%; Pred. No. 63;
CC Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGCCAGAAAT 24
DB 367 AACCCACCAAGAGAGCCAGAAAT 345

RESULT 3
ID ABZ12691 standard; DNA; 2868 BP.
XX
AC ABZ12691;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 496.
XX
XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
OS Arabidopsis thaliana.
XX
PM WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
XX
PR 26-JAN-2001; 2001US-0264647P.
XX
PR 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI) SCRIPPS RBS INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX Harper JF, Kreps J, Wang X, Zhu T;
 PI WPI; 2002-304127/34.
 DR
 XX Identifying a stress condition to which a plant cell has been exposed and
 PT producing plants with increased tolerance to these abiotic stresses.
 XX
 PS Claim 144; SEQ ID NO 496; 577pp + Sequence Listing; English.
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 SQ Sequence 2868 BP; 871 A; 581 C; 682 G; 734 T; 0 U; 0 Other;
 Query Match 82.5%; Score 19.8; DB 6; Length 2868;
 Best Local Similarity 91.3%; Pred. No. 74;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AGCCACCAAGAGAGAGAGAGAGAT 24
 DB 694 AACCCACCAAGAGAGAGAGAGAGAT 672
 RESULT 4
 ADA68110/c
 ID ADA68110 standard; DNA; 2868 BP.
 XX
 AC ADA68110;
 XX
 DT 20-NOV-2003 (first entry)
 DE Arabidopsis thaliana gene, SEQ ID 373.
 XX
 KM Plant; bacterial infection; fungal infection; viral infection; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2003000898-A1.
 PD 03-JAN-2003.
 PF 22-JUN-2001; 2001WO-IB001105.
 PR 22-JUN-2001; 2001WO-IB001105.
 PS (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PA Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
 PI Katagiri F, Qian S, Tao Y, Whitman S, Xie Z, Zhu T, Zou G;
 PI WPI; 2003-175290/17.
 DR
 XX Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.
 XX
 PS Claim 6; SEQ ID NO 373; 899pp; English.
 CC The present invention relates to a method (M1) for identifying genes
 CC involved in plant resistance or response to pathogenic infection. M1

CC comprises identifying a gene whose expression is significantly altered in
 CC the incompatible interaction of plant gene expression relative to
 CC expression of the gene in an uninfected plant, in a mutant plant that
 CC does not express a gene associated with response to pathogenic infection,
 CC or in a corresponding incompatible or compatible interaction. (M1) is
 CC useful for conferring resistance to resistance or tolerance to a plant to
 CC bacterial, fungal or viral infection. The present sequence was used to
 CC illustrate the invention.
 XX
 SQ Sequence 2868 BP; 871 A; 581 C; 682 G; 734 T; 0 U; 0 Other;
 Query Match 82.5%; Score 19.8; DB 7; Length 2868;
 Best Local Similarity 91.3%; Pred. No. 74;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 AGCCACCAAGAGAGAGAGAGAGAT 24
 DB 694 AACCCACCAAGAGAGAGAGAGAGAT 672
 RESULT 5
 AAA52645/c
 ID AAA52645 standard; DNA; 141 BP.
 XX
 AC AAA52645;
 XX
 DT 07-DEC-2000 (first entry)
 DE Eosinophil activating peptide gene 33.
 XX
 KM Eosinophil activation; human; allergy; eosinophilia; cancer;
 KM inflammation; signalling peptide; cell adhesion peptide;
 KM G-protein coupled receptor; secreted protein; cell surface protein; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200032630-A2.
 PD 08-JUN-2000.
 PF 06-DEC-1999; 99WO-US028773.
 PR 04-DEC-1998; 98US-0111006P.
 PS (SEAR) SEARLE & CO G D.
 PI Dotson SB, Ma X;
 PI WPI; 2000-465041/40.
 DR
 XX Novel nucleic acids derived from activated eosinophil cells useful for
 PT treating allergic diseases such as asthma comprises a specific nucleotide
 PT sequence.
 XX
 PS Claim 1; Page 114; 125pp; English.
 CC The present invention relates to a number of nucleotide sequences which
 CC encode proteins involved in the activation of eosinophils (AAA52601-
 CC A52679). Eosinophils are involved in immune reactions, and these genes
 CC and their proteins provide possible targets for new drugs to combat
 CC diseases such as asthma, allergic rhinitis, atopic dermatitis,
 CC anaphylaxis, allergic bronchopulmonary aspergillosis, eczema, psoriasis,
 CC emphysema, leukaemia, lymphomas, ovarian cancer, pneumonia, immune
 CC disorders, some connective tissue disorders, and inflammatory conditions
 CC including septic shock, arthritis, nephritis, inflammatory bowel disease
 CC and Crohn's disease
 XX
 SQ Sequence 141 BP; 17 A; 40 C; 49 G; 35 T; 0 U; 0 Other;
 Query Match 79.2%; Score 19; DB 3; Length 141;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCCACCAAGAGAGACC 19
 |||||
 DB 102 CAGCCACCAAGAGAGACC 84

RESULT 6
 ID ABRK4368 standard; cDNA; 3062 BP.
 AC ABRK4368;
 XX
 DT 14-AUG-2002 (first entry)
 DE Human CDNA differentially expressed in granulocytic cells #939.

Human; B6; granulocytic cell; DNA chip; bacterial infection;
 viral infection; parasitic infection; protozoal infection;
 fungal infection; sterile inflammatory disease; psoriasis;
 rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
 cardiac reperfusion injury; renal reperfusion injury; ARDS;
 adult respiratory distress syndrome; inflammatory bowel disease;
 Crohn's disease; ulcerative colitis; periodontal disease;
 granulocyte activation; chronic inflammation; allergy.

OS Homo sapiens.
 PN WO200226999-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 03-OCT-2001; 2001WO-US030821.
 XX
 PR 03-OCT-2000; 2000US-0237189P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
 DR WPI; 2002-435328/46.
 XX
 PT Detecting granulocyte activation by detecting differential expression of
 genes associated with granulocyte activation, which serves as diagnostic
 markers that is useful for monitoring disease states and drug toxicity.

Claim 1; SEQ ID NO 939; 114pp; English.

The invention relates to detecting (M1) granulocyte (GC) activation
 (GCA), by detecting the level of expression of gene(s) (Gs) identified by
 DNA chip analysis as given in the specification, and comparing the
 expression level to an expression level in an unactivated GC, where
 differential expression of Gs is indicative of GCA. Also included are
 modulating (M2) Gs by contacting GC with an agent that alters the
 expression of at least one gene in Gs; (2) screening (M3) for an agent
 capable of modulating GCA or an inflammation (especially chronic) in a
 tissue, an allergic response in a subject, exposure of a subject to a
 pathogen or sterile inflammatory disease using the gene expression
 profile; (3) detecting (M4) an inflammation (especially chronic) in a
 tissue, an allergic response in a subject, exposure of a subject to a
 pathogen or sterile inflammatory disease, by detecting the level of
 expression in a sample of the tissue of gene(s) from Gs, where the level
 of expression of the gene is indicative of inflammation; (4) treating
 (M5) an inflammation (especially chronic) or in a tissue, an allergic
 response in a subject, exposure of a subject to a pathogen or sterile
 inflammatory disease, by contacting a tissue having inflammation with an
 agent that modulates the expression of gene(s) from Gs in the tissue. M1
 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful
 for screening an agent capable of modulating GCA preferably in an
 inflammation in a tissue; M4 is useful for detecting an inflammation
 (especially chronic) in a tissue, an allergic response in a subject,
 exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
 psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
 cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
 respiratory distress syndrome, inflammatory bowel disease, Crohn's

CC disease, ulcerative colitis, periodontal disease; also bacterial
 CC infection, viral infection, parasitic infection, protozoal infection,
 CC fungal infection and M5 is useful for treating one of the above
 CC conditions. The present sequence represents a gene differentially
 CC expressed in granulocytes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 3062 BP; 547 A; 870 C; 1009 G; 636 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 6; Length 3062;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAGCCACCAAGAGAGACC 19
 |||||
 DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 7
 ID ABR96885/C
 AC ABR96885 standard; DNA; 3062 BP.
 XX
 AC ABR96885;
 XX
 DT 13-AUG-2002 (first entry)
 DE Gene #3383 used to diagnose liver cancer.

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;
 metastatic liver tumour; cytostatic; expression profile; disease state;
 disease progression; drug toxicity; drug efficacy; drug metabolism.

OS Homo sapiens.
 PN WO200229103-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 02-OCT-2001; 2001WO-US030589.
 XX
 PR 02-OCT-2000; 2000US-0237054P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Horne D, Alvares C, Pires-da-Silva S, Vockley JG;
 DR WPI; 2002-426119/45.
 XX
 PT Diagnosing and detecting the progression of liver cancer, hepatocellular
 carcinoma or metastatic liver tumor in a patient, involves detecting the
 PT level of expression of two or more genes in a liver tissue sample.

Claim 1; SEQ ID NO 3383; 298bp; English.

The invention relates to a novel method for diagnosing and detecting the
 progression of liver cancer, hepatocellular carcinoma or metastatic liver
 tumor in a patient, and differentiating metastatic liver cancer from
 CC hepatocellular carcinoma in a patient, involving detecting the level of
 CC expression of two or more genes represented in ABR93503-ABN97455 in a
 CC tissue sample. The method of the invention has hepatotropic, and
 CC cytostatic activity. The method is useful for diagnosing and detecting
 CC the progression of liver cancer, hepatocellular carcinoma and metastatic
 CC liver carcinoma in a patient. The method is useful for identifying
 CC expression profiles which serve as useful diagnostic markers as well as
 CC markers that can be used to monitor disease states, disease progression,
 CC drug toxicity, drug efficacy and drug metabolism. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX

Sequence 3062 BP; 547 A; 870 C; 1009 G; 636 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 6; Length 3062;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 8

ADD18955/C
ID ADD18955 standard; DNA; 3062 BP.

AC ADD18955;
XX

DT 15-JAN-2004 (first entry)

DE Human disease related protein DNA sequence SeqID444.

human; disease state; cytosolic; antiinflammatory; ophthalmological;
antiarteriosclerotic; vulnery; gene therapy;
hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
inflammation; erythropoiesis; glycolysis; gluconeogenesis;
glucose transportation; catecholamine synthesis; iron transport;
nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
inflammatory condition; wound healing; gene; ds.

OS Homo sapiens.
XX

PN WO2003018621-A2.
XX

PD 06-MAR-2003.
XX

PF 23-AUG-2002; 2002WO-GB003892.
XX

PR 23-AUG-2001; 2001GB-00020558.
XX

PR 05-OCT-2001; 2001GB-00024037.
XX

PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX

PI Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX

DR WPI; 2003-290046/28.
XX

DR P-PSDB; ADD18954.
XX

PT New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX

PS Claim 27; SEQ ID NO 444; 424pp; English.
XX

CC This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytosolic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnery activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein encoding DNA sequence of the invention.
XX

SQ Sequence 3062 BP; 547 A; 870 C; 1009 G; 636 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 9; Length 3062;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 9

ABZ68460/C
ID ABZ68460 standard; DNA; 3205 BP.

AC ABZ68460;
XX

DT 22-APR-2003 (first entry)

DE Nucleotide sequence of human NOV1 polypeptide.

human; NOV1; hexokinase 3; splice variant; metabolic disorder; diabetes;
obesity; anorexia; cancer; metastatic melanoma; cancer; enzyme;
neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
immune disorder; systemic lupus erythematosus; haematopoietic disorder;
cirrhosis; transplant; autoimmune disease; allergy; infection; vaccine;
high blood pressure; haemophilia; wasting disorder; gene therapy; gene;
ss.

OS Homo sapiens.
XX

PH Key Location/Qualifiers
XX

FT CDS 75..1148
FT /*tag= a
FT /product= "NOV1"
XX

PN WO2003000918-A2.
XX

PD 03-JAN-2003.
XX

PF 21-JUN-2002; 2002WO-US019650.
XX

PR 21-JUN-2001; 2001US-0299949P.
XX

PR 22-JUN-2001; 2001US-0300290P.
XX

PR 09-AUG-2001; 2001US-0311285P.
XX

PR 05-OCT-2001; 2001US-0327345P.
XX

PR 09-OCT-2001; 2001US-0327892P.
XX

PA (CURA-) CUBAGEN CORP.
XX

PI Grose WM, Alsobrook JP, Lepley DM, Burgees CE, Bader JS;
XX

PI Bansal A, Pena CE, Shinkets RA;
XX

DR WPI; 2003-184053/18.
XX

DR P-PSDB; ABP70634.
XX

PT New NOV-1 polypeptides and polynucleotides, useful for manufacturing a
PT medicament for treating or preventing disorders or syndromes, including
PT metabolic disorders, cancer, neurodegenerative and autoimmune disorders.
XX

PS Claim 21; Page 116; 147pp; English.
XX

CC The present sequence encodes a polypeptide, designated NOV1. NOV1 is a
CC member of the hexokinase 3-like family. It is an alternative splice
CC variant. The NOV-1 polypeptide, nucleic acid or antibody is useful for
CC manufacturing a medicament for treating or preventing disorders or
CC syndromes, including metabolic disorders (e.g. diabetes, obesity, or
CC anorexia), cancer (e.g. metastatic melanoma), cancer-associated
CC disorders, neurodegenerative disorders (e.g. Alzheimer's disease,
CC Parkinson's disease), immune disorders (e.g. systemic lupus
CC erythematosus), haematopoietic disorders, cirrhosis, transplantion,
CC autoimmune disease, allergies, and wasting disorders associated with
CC blood pressure, haemophilia, and various cancers. The polypeptides may be used as immunogen to
CC produce antibodies, as vaccines, and to screen for potential agonist and
CC antagonist compounds. The nucleic acids are also useful in gene therapy,
CC in chromosome mapping, tissue typing, and in forensic identification of a

CC biological sample
XX
SQ Sequence 3205 BP; 571 A; 900 C; 1061 G; 673 T; 0 U; 0 Other;
Query Match 79.2%; Score 19; DB 7; Length 3205;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063
RESULT 10
AB268462/c
ID AB268462 standard; DNA; 3205 BP.
XX
AC AB268462;
XX
DT 22-APR-2003 (first entry)
XX
DE Nucleotide sequence of human NOV1 variant SNP1.
XX
KW Human; NOV1; hexokinase 3; splice variant; metabolic disorder; diabetes;
KW obesity; anorexia; cancer; metastatic melanoma; cancer; enzyme;
KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
KW immune disorder; systemic lupus erythematosus; haematopoietic disorder;
KW cirrhosis; transplant; autoimmune disease; allergy; infection; vaccine;
KW high blood pressure; haemophilia; wasting disorder; gene therapy;
KW single nucleotide polymorphism; SNP; ss.
XX
OS Homo sapiens.
XX
PN WO2003000918-A2.
XX
PD 03-JAN-2003.
XX
PF 21-JUN-2002; 2002WO-US019650.
XX
PR 21-JUN-2001; 2001US-0299949P.
XX
PR 22-JUN-2001; 2001US-0300290P.
XX
PR 09-AUG-2001; 2001US-0311285P.
XX
PR 05-OCT-2001; 2001US-0327345P.
XX
PR 09-OCT-2001; 2001US-0327892P.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Grosse WM, Alsobrook JP, Lepley DM, Burgess CE, Bader JS;
PI Bansal A, Pena CE, Shimkets RA;
XX
XX WPI; 2003-184053/18.
XX
PT New NOV-1 polypeptides and polynucleotides, useful for manufacturing a
PT medicament for treating or preventing disorders or syndromes, including
PT metabolic disorders, cancer, neurodegenerative and autoimmune disorders.
XX
PS Claim 46; Page 121; 147pp; English.
XX
CC The present sequence represents a variant of NOV1, comprising a single
CC nucleotide polymorphism (SNP). NOV1 is a member of the hexokinase 3-like
CC family. It is an alternative splice variant. The NOV-1 polypeptide,
CC nucleic acid or antibody is useful for manufacturing a medicament for
CC treating or preventing disorders or syndromes, including metabolic
CC disorders (e.g. diabetes, obesity, or anorexia), cancer (e.g. metastatic
CC melanoma), cancer-associated disorders, neurodegenerative disorders (e.g.
CC Alzheimer's disease, Parkinson's disease), immune disorders (e.g.
CC systemic lupus erythematosus), haematopoietic disorders, cirrhosis,
CC transplantation, autoimmune disease, allergies, viral/bacterial/parasitic
CC infections, high blood pressure, haemophilia, and wasting disorders
CC associated with chronic and various cancers. The polypeptides may be used
CC as immunogen to produce antibodies, as vaccines, and to screen for
CC potential agonist and antagonist compounds. The nucleic acids are also
CC useful in gene therapy, in chromosome mapping, tissue typing, and in

CC forensic identification of a biological sample
XX
SQ Sequence 3205 BP; 571 A; 901 C; 1061 G; 672 T; 0 U; 0 Other;
Query Match 79.2%; Score 19; DB 7; Length 3205;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063
RESULT 11
ADCl0127/c
ID ADCl0127 standard; DNA; 3205 BP.
XX
AC ADCl0127;
XX
DT 18-DEC-2003 (first entry)
XX
DE Human NOVX polypeptide coding sequence SEQ ID NO: 147.
XX
KW ds; gene; cytosolic; antidiabetic; anorectic; cerebroprotective;
KW neuroprotective; antiinflammatory; gene therapy; antisense therapy;
KW thymometric; NOVX; pathology; cancer; diabetes; obesity;
KW endocrine disorder; CNS disorder; inflammatory disorder;
KW chromosome mapping; tissue typing; predictive medicine.
XX
OS Homo sapiens.
XX
PN WO2003000842-A2.
XX
XX
PD 03-JAN-2003.
XX
PF 04-JUN-2002; 2002WO-US017443.
XX
PR 04-JUN-2001; 2001US-0295607P.
XX
PR 04-JUN-2001; 2001US-0295611P.
XX
PR 06-JUN-2001; 2001US-0296404P.
XX
PR 06-JUN-2001; 2001US-0296418P.
XX
PR 07-JUN-2001; 2001US-0296575P.
XX
PR 11-JUN-2001; 2001US-0297414P.
XX
PR 12-JUN-2001; 2001US-0295573P.
XX
PR 12-JUN-2001; 2001US-0297567P.
XX
PR 14-JUN-2001; 2001US-0298285P.
XX
PR 15-JUN-2001; 2001US-0298528P.
XX
PR 18-JUN-2001; 2001US-0299133P.
XX
PR 19-JUN-2001; 2001US-0299230P.
XX
PR 21-JUN-2001; 2001US-0299949P.
XX
PR 22-JUN-2001; 2001US-0300177P.
XX
PR 26-JUN-2001; 2001US-0300883P.
XX
PR 28-JUN-2001; 2001US-0301530P.
XX
PR 28-JUN-2001; 2001US-0301550P.
XX
PR 03-JUL-2001; 2001US-0302951P.
XX
PR 31-JUL-2001; 2001US-0308890P.
XX
PR 14-SEP-2001; 2001US-0322297P.
XX
PR 25-SEP-2001; 2001US-0324669P.
XX
PR 03-DEC-2001; 2001US-0337477P.
XX
PR 14-DEC-2001; 2001US-0341562P.
XX
PR 21-FEB-2002; 2002US-0358656P.
XX
PR 22-FEB-2002; 2002US-0358978P.
XX
PR 22-FEB-2002; 2002US-0359034P.
XX
PR 22-FEB-2002; 2002US-0359035P.
XX
PR 22-FEB-2002; 2002US-0359121P.
XX
PR 27-FEB-2002; 2002US-0359649P.
XX
PR 01-MAR-2002; 2002US-0360858P.
XX
PR 12-MAR-2002; 2002US-0363430P.
XX
PR 12-MAR-2002; 2002US-0363676P.
XX
PR 10-APR-2002; 2002US-0371346P.
XX
PR 10-MAY-2002; 2002US-0379444P.
XX
PR 04-JUN-2002; 2002US-00379444.

XX (CURA-) CURAGEN CORP.
PA Agee M., Anderson DW, Berghs C, Casman SJ, Catterton E;
XX DiPippo VA, Edinger SR, Eisen A, Ellerman K, Gangolli EA;
PI Gerlach VL, Gorman L, Guo X, Herrmann JL, Hyatt T, Ji W, Kekuda R;
PI Khramtsov NV, Li L, Liu X, Malyankar UM, Miller CE, Miller I;
PI Ort T, Padigaru M, Paturajan M, Pena CE, Rastelli L, Rieger DK;
PI Rothenberg ME, Shenoy SG, Shinkets RA, Sultison G, Spaderna SK;
PI Spyrek KA, Stone DJ, Vernet CAM, Zhong H, Zhong W, Alsobrook JP;
PI Burgess CE, Lepley DM;
XX MPI; 2003-210149/20.
DR P-PSDB; ADC10128.
XX
XX New isolated NOVX polypeptides and nucleic acid molecules useful for
PT treating, preventing and diagnosing pathological conditions with NOVX-
PT associated disorders, such as cancer, obesity, diabetes and inflammatory
PT or CNS diseases.
XX
XX Claim 20; SEQ ID NO 147; 772pp; English.
XX
XX The invention relates to novel isolated polypeptides, mature form of the
CC polypeptide, a sequence that is 95% identical to the polypeptide or the
CC polypeptide comprising one or more conservative substitutions. The NOVX
CC polypeptide is useful for treating or preventing a pathology associated
CC with the polypeptide e.g. disorders associated with aberrant expression
CC or activity of the polypeptide, such as cancer, diabetes, obesity, and
CC endocrine, CNS and inflammatory disorders. They can also be used in
CC various detection and screening assays, chromosome mapping, tissue typing
CC and predictive medicine. This sequence corresponds to the coding sequence
CC for one of the polypeptides of the invention.
XX
SQ Sequence 3205 BP; 571 A; 900 C; 1061 G; 673 T; 0 U; 0 Other;
XX
XX
XX Query Match 79.2%; Score 19; DB 9; Length 3205;
XX Best Local Similarity 100.0%; Pred. NO. 1.6e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CAGCCACCAAGAGAGGCC 19
DB 1081 CAGCCACCAAGAGAGGCC 1063
XX
XX
XX RESULT 12
XX AAV00090/c
XX ID AAV00090 standard; cDNA; 3692 BP.
XX
XX AAV00090;
XX
XX 17-MAR-1998 (first entry)
XX
XX Rat hexokinase III encoding cDNA.
XX
XX Yeast; trehalose-6-phosphate synthase; hexokinase; ribozyme; stimulator;
XX Insulin; glucose; diabetes; ss.
XX
XX Rattus sp.
XX
XX
XX Key Location/Qualifiers
XX FT CDS 81..2855
XX FT /*tag= a
XX FT /product= "Hexokinase_III"
XX
XX WO9726357-A1.
XX
XX 24-JUL-1997.
XX
XX 17-JAN-1997; 97WO-US000787.
XX
XX 19-JAN-1996; 96US-00588983.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX
XX

PA (BETA-) BETAGENE INC.
XX
XX Newgard CB, Han H, Thigpen AE, Normington KD;
PI
XX MPI; 1997-385343/35.
XX P-PSDB; AAM37430.
XX
XX Mammalian cell with reduced activity of low Km hexokinase - caused by
PT specific ribozyme or stimulator of trehalose-6-phosphate production,
PT particularly for in vitro or in vivo insulin production.
XX
XX Disclosure; Page 195-198; 265pp; English.
XX
XX A mammalian cell has been developed comprising an effective amount of a
CC low Km hexokinase-inhibitor selected from: (a) an agent that stimulates
CC production of trehalose-6-phosphate (T6P); or (b) a ribozyme specific for
CC low Km hexokinase. The present sequence encodes rat hexokinase III. The
CC cells are particularly used to produce insulin, in response to glucose or
CC other secretagogues, either in vitro or in vivo (for treating diabetes),
CC but may also be used to produce many other therapeutic proteins, e.g.
CC from a gene under control of the insulin promoter which is therefore
CC responsive to glucose. Growth-inhibited cells (having altered hexokinase
CC activity) are used to produce proteins, e.g. insulin or antibodies, in
CC vivo or in vitro. Reduction in low Km hexokinase activity provides cells
CC in which insulin secretion is induced at glucose concentrations closer to
CC the normal range than in the parent cell (nearly homeostatic secretion).
CC Implanted cells of reduced low Km hexokinase activity are expected to
XX survive longer in the host
XX
SQ Sequence 3692 BP; 821 A; 969 C; 1112 G; 790 T; 0 U; 0 Other;
XX
XX
XX Query Match 79.2%; Score 19; DB 2; Length 3692;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e+02;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CAGCCACCAAGAGAGGCC 19
DB 1087 CAGCCACCAAGAGAGGCC 1069
XX
XX
XX RESULT 13
XX AAV00160/c
XX ID AAV00160 standard; cDNA; 3692 BP.
XX
XX AAV00160;
XX
XX 17-MAR-1998 (first entry)
XX
XX Rat hexokinase III encoding cDNA.
XX
XX Hexokinase; competitive enzyme; inhibitor; insulin; diabetes; B cell;
XX glucose; glucokinase; ss.
XX
XX Rattus sp.
XX
XX
XX Key Location/Qualifiers
XX FT CDS 81..2855
XX FT /*tag= a
XX FT /product= "Hexokinase_III"
XX
XX WO9726322-A2.
XX
XX 24-JUL-1997.
XX
XX 17-JAN-1997; 97WO-US000786.
XX
XX 19-JAN-1996; 96US-00588976.
XX
XX (TEXA) UNIV TEXAS SYSTEM.
XX (BETA-) BETAGENE INC.
XX (UNMS) UNIV MICHIGAN STATE.
XX
XX Newgard CB, Han H, Becker TC, Wilson JB;
PI

XX MPI: 1997-385327/35.
 DR P-PSDB: AAM37443.
 XX Mammalian cell with reduced activity of low Km hexokinase - caused by
 PT competitive enzyme inhibitor, particularly an insulin secreting cell for
 PT in vitro or in vivo insulin production.
 XX
 PS Disclosure: Page 195-198; 254pp; English.
 XX
 CC A mammalian cell has been developed which includes enough of a
 CC competitive inhibitor of low Km (Michaelis constant) hexokinase to reduce
 CC the hexokinase activity in the cell. The present sequence encodes rat
 CC hexokinase III. The cells are particularly used to produce insulin, in
 CC response to glucose or other secretagogues, either in vitro or in vivo
 CC (for treating diabetes), but may also be used to produce many other
 CC therapeutic proteins, e.g. from a gene under control of the insulin
 CC promoter and thus responsive to glucose. Inhibition of the inhibitor can
 CC be used more generally to reduce the growth rate of cells, e.g.
 CC hydridomas that produce antibodies
 XX
 SQ Sequence 3692 BP; 821 A; 969 C; 1112 G; 790 T; 0 U; 0 Other;
 Query Match 79.2%; Score 19; DB 2; Length 3692;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCACCAAGAGAGACC 19
 Db 1087 CAGCCACCAAGAGAGACC 1069
 RESULT 14
 ID ABT42065/C
 XX ABT42065 standard; DNA; 3692 BP.
 AC ABT42065;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Toxicity modelling related rat gene SEQ ID No 1767.
 XX
 KM Toxic effect; gene expression profile; renal toxicity; toxicity marker;
 KM database; drug screening; toxicity assay; rat; ds.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200295000-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 22-MAY-2002; 2002MO-US016173.
 XX
 PR 22-MAY-2001; 2001US-0292335P.
 PR 13-JUN-2001; 2001US-0297523P.
 PR 19-JUN-2001; 2001US-0298925P.
 PR 10-JUL-2001; 2001US-0303807P.
 PR 10-JUL-2001; 2001US-0303808P.
 PR 10-JUL-2001; 2001US-0303810P.
 PR 28-AUG-2001; 2001US-0315047P.
 PR 27-SEP-2001; 2001US-0324928P.
 PR 22-OCT-2001; 2001US-0330462P.
 PR 01-NOV-2001; 2001US-0330867P.
 PR 21-NOV-2001; 2001US-0331805P.
 PR 06-DEC-2001; 2001US-0336144P.
 PR 19-DEC-2001; 2001US-0340873P.
 PR 21-FEB-2002; 2002US-0357842P.
 PR 21-FEB-2002; 2002US-0357843P.
 PR 15-MAR-2002; 2002US-0357844P.
 PR 08-APR-2002; 2002US-0370144P.
 PR 08-APR-2002; 2002US-0370206P.
 PR 08-APR-2002; 2002US-0370247P.

PR 17-APR-2002; 2002US-0372794P.
 PR 21-APR-2002; 2002US-0371679P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
 XX MPI: 2003-148464/14.
 DR
 XX
 XX Predicting at least one toxic effect of a compound, useful for toxicity
 PT modeling, comprises preparing a gene expression profile of a tissue or
 PT cell sample exposed to the compound, and comparing the gene expression
 PT profile to a database.
 XX
 PS Example 4; Page; 446pp; English.
 XX
 CC The invention relates to a novel method of predicting at least one toxic
 CC effect of a compound. The method comprises a gene expression profile of a
 CC tissue or cell sample exposed to the compound, and comparing the gene
 CC expression profile to a database comprising at least part of the data or
 CC information given in the specification. The methods are useful for
 CC predicting at least one toxic effect of a compound, predicting the
 CC progression of a toxic effect of a compound, predicting the renal
 CC toxicity of a compound, or identifying toxicity markers in tissues or
 CC cells exposed to known renal toxin. The genes are useful as toxicity
 CC markers in drug screening and toxicity assays, in monitoring disease or
 CC physiological states, or disease progression. This polynucleotide
 CC represents a rat DNA sequence relating to the toxic effect database
 CC described in the specification. NOTE: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from the World Intellectual Property
 CC Organization
 XX
 SQ Sequence 3692 BP; 821 A; 969 C; 1112 G; 790 T; 0 U; 0 Other;
 Query Match 79.2%; Score 19; DB 7; Length 3692;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CAGCCACCAAGAGAGACC 19
 Db 1087 CAGCCACCAAGAGAGACC 1069
 RESULT 15
 ID ADB58419/C
 XX ADB58419 standard; DNA; 3692 BP.
 AC ADB58419;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE Toxicity-related gene, SEQ ID 3445.
 XX
 KM Toxic; toxin; gene expression profile; hepatotoxicity; liver;
 KM drug screening; toxicity assay; ds.
 XX
 OS Unidentified.
 XX
 PN WO2003064624-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 31-JAN-2003; 2003MO-US003194.
 XX
 PR 31-JAN-2002; 2002US-00060087.
 PR 15-MAR-2002; 2002US-0364045P.
 PR 15-MAR-2002; 2002US-0364055P.
 PR 30-DEC-2002; 2002US-0436643P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;

XX
DR WPI; 2003-689530/65.

XX
PT Predicting a toxic effect of a compound, useful in identifying toxicity
PT markers in liver tissues or cells for drug screening and toxicity assays,
PT comprises preparing gene expression profile of tissue or cells exposed to
PT the compound.

PS
XX Claim 1; SEQ ID NO 3445; 1156bp; English.

CC The present invention relates to a method for predicting a toxic effect
CC of a compound. The method comprises preparing a gene expression profile
CC of a tissue or cell sample exposed to the compound, and comparing the
CC gene expression profile to a database comprising SEQ ID 1-4925, where
CC differential expression of the gene indicates at least one toxic effect.
CC The method is useful for predicting at least one toxic effect of a
CC compound, predicting hepatotoxicity or the progression of a toxic effect
CC of a compound, identifying an agent that modulates the onset or
CC progression of a toxic response, predicting the cellular pathways that a
CC compound modulates in a cell, and identifying an agent that modulates at
CC least one activity of a protein. The method and compositions of the
CC present invention using a database of genes having liver toxin-induced
CC differential expression, are useful in identifying toxicity markers in
CC liver tissues or cells for drug screening and toxicity assays. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 3692 BP; 821 A; 969 C; 1112 G; 790 T; 0 U; 0 Other;

Query Match 79.2%; Score 19; DB 9; Length 3692;

Best Local Similarity 100.0%; Pred. No. 1.7e+02;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGACCC 19

DB 1087 CAGCCACCAAGAGACCC 1069

Search completed: July 30, 2004, 20:33:04
Job time : 386 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2004, 19:11:31 ; Search time 2503 Seconds
(without alignments)

415.594 Million cell updates/sec

Title: US-09-831-272-7

Perfect score: 24

Sequence: 1 cagccaccaagagagaccagcaat 24

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank
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2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_scs: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_scs: *
28: em_un: *
29: em_vl: *
30: em_hg_hum: *
31: em_hg_in: *
32: em_hg_other: *
33: em_hg_mus: *
34: em_hg_pln: *
35: em_hg_rod: *
36: em_hg_man: *
37: em_hg_vtl: *
38: em_sy: *
39: em_hgo_hum: *
40: em_hgo_mus: *
41: em_hgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	24	AX025607	AX025607 Sequence
2	24	100.0	3549	AF239835	AF239835 Sequence
3	19.8	82.5	2868	AX050801	AX050801 Sequence
4	19.8	82.5	2868	AX651563	AX651563 Sequence
5	19.8	82.5	2962	AY133782	AY133782 Arabidops
6	19.8	82.5	3107	AF081202	AF081202 Arabidops
7	19.8	82.5	3295	AF088801	AF088801 Lilium lo
8	19.8	82.5	3383	AY080601	AY080601 Arabidops
9	19.8	82.5	81843	AL672309	AL672309 Mouse DNA
10	19.8	82.5	91071	AC002339	AC002339 Arabidops
11	19.4	80.8	813	BY071807	BY071807 S212P6764
12	19.4	80.8	173763	AC134552	AC134552 Mus muscu
13	19.4	80.8	183349	AC087416	AC087416 Mus muscu
14	19.4	80.8	213625	AL805918	AL805918 Mouse DNA
15	19.2	80.0	1603	VCCYNA	X69193 V. carduncul
16	19.2	80.0	130709	AF082029	AF082029 Hemerocal
17	19.2	80.0	189891	AC119058	AC119058 Papio anu
18	19.2	80.0	191132	AC126895	AC126895 Rattus no
19	19.2	80.0	192082	AL591490	AL591490 Mouse DNA
20	19.2	80.0	206145	BX813306	BX813306 Mus muscu
21	19.2	80.0	214393	BX537302	BX537302 Mouse DNA
22	19.2	80.0	226299	AC112320	AC112320 Rattus no
23	19.2	80.0	247220	AC073807	AC073807 Mus muscu
24	19.2	80.0	255871	AC095418	AC095418 Rattus no
25	19.2	80.0	260367	AC099427	AC099427 Rattus no
26	19.2	79.2	3062	AX410736	AX410736 Sequence
27	19.2	79.2	3073	HSU51333	U51333 Human hexok
28	19.2	79.2	3073	BC028129	BC028129 Homo sapi
29	19.2	79.2	3592	AR068840	AR068840 Sequence
30	19.2	79.2	3592	AR070140	AR070140 Sequence
31	19.2	79.2	3692	RNU73859	U73859 Rattus norv
32	19.2	79.2	121282	AC027318	AC027318 Homo sapi
33	19.2	79.2	166534	AC034209	AC034209 Homo sapi
34	19.2	79.2	168168	AC012283	AC012283 Homo sapi
35	19.2	79.2	220152	AC119372	AC119372 Rattus no
36	19.2	79.2	220152	AC139592	AC139592 Rattus no
37	19.2	79.2	231407	AC095489	AC095489 Rattus no
38	19.2	79.2	267520	GI7829	GI7829 human STS
39	18.8	78.3	2228	AY069309	AY069309 Drosophila
40	18.8	78.3	2452	BC044275	BC044275 Xenopus 1
41	18.8	78.3	2999	AY128892	AY128892 Arabidops
42	18.8	78.3	3335	AF081203	AF081203 Arabidops
43	18.8	78.3	3548	AY093052	AY093052 Arabidops
44	18.8	78.3	73181	AC117455	AC117455 Homo sapi
45	18.8	78.3	73181	AC117455	AC117455 Homo sapi

ALIGNMENTS

RESULT 1
AX025607
LOCUS AX025607 24 bp DNA linear PAT 16-SEP-2000
SEQUENCE 7 from Patent WO029592.
AX025607
VERSION AX025607.1 GI:10187275
KEYWORDS
SOURCE
ORGANISM
Petroselinum crispum (parsley)
Petroselinum crispum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Apiales; Apiaceae; Apioidae; apioid
superclade; Apium clade; Petroselinum.
REFERENCE
1 Logemann, E., Somsch, I., Hahlbrock, K., Kirsch, C. and Rushton, P.

TITLE Chimeric promoters capable of mediating gene expression in plants
JOURNAL upon pathogen infection and uses thereof
Patent: WO 0029592-A 7 25-MAY-2000;
MAX PLANCK GESELLSCHAFT (DE) ; LOGEMANN ELKE (DE) ; SOMSSICH IMRE
(DE) ; HAHNBROCK KLAUS (DE) ; KIRSCH CHRISTOPH (DE) ; RUSHTON PAUL
(GB)

FEATURES
SOURCE location/Qualifiers
1..24
/organism="Petroselinum crispum"
/mol_type="unassigned DNA"
/db_xref="taxon:4043"

ORIGIN
Query Match 100.0%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.31;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCCACCAAGAGAGAGCCAGAAAT 24
1 CAGCCACCAAGAGAGAGCCAGAAAT 24

Db 1 CAGCCACCAAGAGAGAGCCAGAAAT 24

RESULT 2 3549 bp DNA linear PLN 22-OCT-2000
AF239835
LOCUS Petroselinum crispum fatty acid desaturase/hydroxylase-like protein
DEFINITION EL17.1 (EL17.1) gene, complete cds; and fatty acid
desaturase/hydroxylase-like protein EL17.2 (EL17.2) gene, partial
cds.
AF239835
AF239835.1 GI:10945374
Petroselinum crispum (parsley)
Petroselinum crispum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Apiales; Apiaceae; Apioideae; aploid
superclade; Apium clade; Petroselinum.
1 (bases 1 to 3549)
Kirsch, C., Takamiya-Wik, M., Schmelzer, E., Hahnbrock, K. and
Somssich, I.E.
A novel regulatory element involved in rapid activation of parsley
EL17 gene family members by fungal elicitor or pathogen infection
Mol. Plant Pathol. 1 (4), 243-251 (2000)
2 (bases 1 to 3549)
Kirsch, C., Takamiya-Wik, M. and Somssich, I.E.
Direct Submision
Submitted (29-FEB-2000) Biochemistry, Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany

FEATURES
SOURCE location/Qualifiers
1..3549
/organism="Petroselinum crispum"
/mol_type="genomic DNA"
/db_xref="taxon:4043"
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380..1782
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EL17.1"
551..1702
/gene="EL17.1"
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EL17.1"
/protein_id="AA024521.1"
/db_xref="GI:10945375"

gene
mRNA
CDS

RESULT 4 2868 bp DNA linear PAT 27-MAR-2003
AX651563/c
LOCUS Arabidopsis thaliana
DEFINITION Sequence 373 from Patent WO03000898.
ACCESSION AX651563
VERSION AX651563.1 GI:29154381
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

TERRKOITVDAIILAVIYGLRYLVILKGFAMVFCYGGPLLVNMMFTLILNHT
HSPVRYDSTREMDLFGALCTYRDGIILNKVPHNVGNHACHITSMIPHYGLEAT
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3218..>3549
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3218..>3549
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3384..>3549
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/db_xref="GI:10945376"
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FKSLVTSFRY"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CAGCCACCAAGAGAGAGCCAGAAAT 24
1 CAGCCACCAAGAGAGAGCCAGAAAT 3052

Db 3029 CAGCCACCAAGAGAGAGCCAGAAAT 3052

RESULT 3 2868 bp DNA linear PAT 27-SEP-2002
AX505801/c
LOCUS Arabidopsis thaliana
DEFINITION Sequence 496 from Patent WO0216655.
ACCESSION AX505801
VERSION AX505801.1 GI:23387038
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
Harper, J. F., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of use of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 496 28-SEP-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

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SOURCE location/Qualifiers
1..2868
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/db_xref="taxon:3702"

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Query Match 82.5%; Score 19.8; DB 6; Length 2868;
Best Local Similarity 91.3%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 AGCCACCAAGAGAGAGCCAGAAAT 24
694 AACACCAAGAGAGAGCCAGAAAT 672

Db 694 AACACCAAGAGAGAGCCAGAAAT 672

RESULT 4 2868 bp DNA linear PAT 22-MAR-2003
AX651563
LOCUS Arabidopsis thaliana
DEFINITION Sequence 373 from Patent WO03000898.
ACCESSION AX651563
VERSION AX651563.1 GI:29154381
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

JOURNAL Plant Physiol. 122 (1), 35-48 (2000)
 MEDLINE 20098711
 PUBLISHED 10631247
 REFERENCE 2 (bases 1 to 3107)
 AUTHORS Klahre, U. and Chua, N.-H.
 TITLE Direct Submission
 JOURNAL Submitted (31-JUL-1998) Laboratory of Plant Molecular Biology, The Rockefeller University, 1230 York Avenue, New York, NY 10021, USA

FEATURES
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 /db_xref="taxon:3702"
 /chromosome="II"
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 /gene="VILN2"
 1..2931
 /note="VILN2"
 /note="Atvillin; similar to protein encoded by T11A7.16 gene"
 /codon_start=1
 /product="villin 2"
 /protein_id="AAC31606.1"
 /db_xref="GI:3415115"
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 TYVLQTTONGAGVLPDIHFMIGKDTSDPAGTAIVTVLDAVLGRAVQHRVIG
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 NHDVFLIDTEKTYIQFGANSNIQERAKALEVQYLKDKYBGTCTVALVDGKLDT
 BSDGAEFWLFGFAPIGRKVANDDIPESTPRLYCIITDGKMEPIDGSLSKMLN
 TKCYLIDCGAEIYIWMGVQVDRKKAQSAEFLSENPKATVTRVIOGVESH
 KSNPDSWPSGATPGNEBGRKVAALLKQGVGKIGAKGAPVNEIPLPLESGKL
 EAWYVNGKVTPLPREDKIKYSGDCYIVLYTHSGEKDEPLSCWKGKSLPEDD
 TAILATMSLSLKRPIVQGRITYGKEKPPQVALPQPMVILKGLSSGYKSMSESS
 TDEITYTESIALVOVSGVHNNAVQETVATSLNSYECFLQSGTSMFLMHQNSST
 HEOLELAKVAEFLKPGITLLKAKGKESTFTWFGALGKQNFSTKASSETIRPDLF
 SFAPNRGFEVBEIYNFADDLTEDIPLDTHAEVFWGQCYEPEKQTFEFIGQK
 YIDLASLEGHPVPIYKINEGNEPCFTTFPSMDATKATVOGNSFGKSLFEGH
 HVVDKSGNGOGIROPABALANSAFNSNSRPAVSQRIINSHDGRORABALA
 ALSAFNSSSSTKSPPPRFVGTSGASORAAVAALSOIVIAENKSPDTSPPRRST
 SSNPADIPLEADDEBASVAGLEAKSEESVPADETAKEQTEGQSEIQQPG
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 FDLF"

ORIGIN
 Query Match 82.5%; Score 19.8; DB 8; Length 3107;
 Best Local Similarity 91.3%; Pred. No. 52;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGACCAGAAAT 24
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 Db 694 AACCCAAAGAGACCAGAAAT 672

RESULT 7
 AF088901/c 3295 bp mRNA linear PLN 22-FEB-2000
 LOCUS Lilium longiflorum actin bundling protein ABP135 (Y5-7) mRNA,
 DEFINITION complete cds.
 ACCESSION AF088901
 VERSION AF088901.1 GI:5880463
 KEYWORDS
 SOURCE
 ORGANISM
 Lilium longiflorum (trumpet lily)
 Lilium longiflorum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
 Lilium
 1 (bases 1 to 3295)
 REFERENCE
 AUTHORS Vidal, L., Yokota, E., Cheung, A., Shimmen, T. and Hepler, P. K.
 TITLE The 135 kDa actin-bundling protein from Lilium longiflorum pollen
 JOURNAL Protoplasma 209, 283-291 (1999)
 REFERENCE 2 (bases 1 to 3295)

AUTHORS Vidal, L., Yokota, E., Cheung, A., Wu, H. M., Shimmen, T. and
 Hepler, P. K.
 TITLE Direct Submission
 JOURNAL Submitted (31-AUG-1998) Biology, University of Massachusetts,
 Morrill Science Center, Amherst, MA 01003, USA

FEATURES
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 Location/Qualifiers
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 /gene="Y5-7"
 123..3020
 /note="Y5-7"
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 /protein_id="AAD54660.1"
 /db_xref="GI:5880464"
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 SLNHDVFLIDTEKTYIQFGANSNIQERAKALEVQYLKDKYBGTCTVALVDGKLDT
 BSDGAEFWLFGFAPIGRKVANDDIPESTPRLYCIITDGKMEPIDGSLSKMLN
 ENNKCYLIDCGAEIYIWMGVQVDRKKAQSAEFLSENPKATVTRVIOGVESH
 RTPKSNESMPLGASGTSGEBGRKVAALLKQGVGKIGAKGAPVNEIPLPLESGKL
 TGTGTEWLIGSGATPVPQREIKKPYSGDCYIVLYTHSGEKDEPLSCWKGKSLPEDD
 DDQIMARKTASMSKNSLKRPIVQGRITYGKEKPPQVALPQPMVILKGLSSGYKSLKLA
 DKNLINDTYTESIALVOVSGVHNNAVQETVATSLNSYECFLQSGTSMFLMHQNSST
 NASTVEEQQAARVAEFLKPGVYLKAKGKESTFTWFGALGKQNSYKPKDAOESTVD
 PLYVCEFGNKGKLEVEVNFASODDLTEDIPLDTHAEVFWGQCYEPEKQTFEFIGQK
 IGOKYIDLATTLBELSPDVLKYTESNEBCFPAYPSMDGTAKAVOGNSFEKKVAD
 IGSAPFAPEGDSGNSNNSHGPORABALAAALSAFNSNSRPAVSQRIINSHDGRORABALA
 AAVAAALSTVLTAEQKQKMSFTTKRSRSPSPPIVDKMSSESGSKSEETNRSS
 VEWDVDTPLTEADDEBASVAGLEAKSEESVPADETAKEQTEGQSEIQQPG
 SSNPADIPLEKREBAYLSBEEFQSEVGIKEAFRNMLPRWKDILKKK FDLF"

ORIGIN
 Query Match 82.5%; Score 19.8; DB 8; Length 3295;
 Best Local Similarity 91.3%; Pred. No. 52;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGACCAGAAAT 24
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 Db 822 AGCCACCAAGAGACCAGAAAT 800

RESULT 8
 AY080601/c 3383 bp mRNA linear PLN 18-SEP-2002
 LOCUS Arabidopsis thaliana putative villin 2 protein (At2g41740) mRNA,
 DEFINITION complete cds.
 ACCESSION AY080601
 VERSION AY080601.1 GI:19310557
 KEYWORDS
 SOURCE
 ORGANISM
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 1 (bases 1 to 3383)
 REFERENCE
 AUTHORS Yamada, K., Iju, S. X., Sakano, H., Pham, P. K., Banh, J., Chung, M. K.,
 Goldsmith, A. D., Lee, J. M., Quach, H. L., Toriumi, M., Yu, G., Bowser, L.,
 Carminci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
 Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T.,
 Satou, M., Seki, M., Shim, P., Southwick, A., Shinzaki, K.,

TITLE
JOURNAL
REFERENCE
AUTHORS

Davis, R.W., Becker, J.R. and Theologis, A.
Arabidopsis Full Length cDNA Clones
2 (bases 1 to 3383)
Yamada, K., Banb, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carrinchi, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Becker, J.R. and Theologis, A.
Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA') Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carrinchi, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

TITLE
JOURNAL
COMMENT

The Salik, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada, K., Banb, J.,
Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J.,
Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shim, P.,
Southwick, A., Davis, R.W., Becker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)
contributed equally to this work as pfs.

FEATURES
source

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to Genbank.
Location/Qualifiers
1..3383
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
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204..3134
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/db_xref="GI:19310558"

gene
5'UTR
CDS

3'UTR
ORIGIN

Query Match 82.5%; Score 19.8; DB 8; Length 3383;
Best Local Similarity 91.3%; Pred. No. 52;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 AGCCACCAAGAGACCCAGAT 24
897 AACGACCAAGAGACCCAGAT 875

RESULT 9
AL672309
LOCUS
DEFINITION
Accession
AL672309.8 GI:21261900
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
Submitted (28-MAY-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humgen@anger.ac.uk Clone requests: clonequest@sanger.ac.uk
On May 29, 2002 this sequence version replaced gi:20338547.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr; TrEMBL; Wp; WormRep; Information on the WormRep
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormrep RP23-466J17 is
from the RPI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6.

FEATURES
source

1..81843
/organism="Mus musculus"
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/db_xref="taxon:10090"
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ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 81843;
Best Local Similarity 91.3%; Pred. No. 57;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 CAGCCACCAAGAGACCCAGAA 23
21198 CAGCCACCAAGAGACCCAGAA 21220

RESULT 10
AC002339/c 91071 bp DNA linear PLN 11-MAR-2002
LOCUS Arabidopsis thaliana chromosome 2 clone T1A7 map C1C11C08,
DEFINITION complete sequence.
ACCESSION AC002339
VERSION AC002339.3 GI:20196889
KEYWORDS HTG.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Buxarvota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis;
1 (bases 1 to 91071)
REFERENCE Rounsley,S.D., Lin,X., Ketchum,K.A., Crosby,M.L., Brandon,R.C.,
AUTHORS Spriggs,T.A., Mason,T.M., Kerlavage,A.R., Adams,M.D.,
Somerville,C.R. and Venter,J.C.
Unpublished
2 (bases 1 to 91071)
Lin,X.
REFERENCE Direct Submission
AUTHORS Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 91071)
Town,C.D. and Kaul,S.
REFERENCE Direct Submission
AUTHORS Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
JOURNAL Medical Center Dr., Rockville, MD 20850, USA, cdowm@icr.org
COMMENT On Apr 18, 2002 this sequence version replaced gi:6598350.
FEATURES
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/mol_type="genomic DNA"
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(U90439:82778..95824)."
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OKPAPFEMLRPAASENSRSSYSLHEDSGRLTEPMSNTITFMSQNGEYKKKKKNI
CAVLTSBALTELDODLRKPVMSVGEHDNTYKRFRLRDRGLRMTSMNSRRTM
KPVQAVENQCKFATCGSVCSFSSSGYTECNCFNFAVSVDKCLVAPQPCCKL
GNNWKFNLDELXGIVPANDSVISQISQCRCKICLNSACTAVVTYDGSPOCRMK
TRYLSGSDPSLSISVYKTCIDPIAVDPNVNSKSPVTYKSHSICIPCLVGTSTT
LVLFQGLGIVYVYRRKKLAKKARFSKATPKGVMIPSVDEIYAMTDPPNNI
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CGNLLGDLLEAKLTGFGCAADKVDDEKVTVALITGRIYEPGVSSVMVREWI
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complement(3329..5857)
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/note="synonym: T1A7.23; supported by cDNA:

mRNA
gi.7861794.gb.AF204675.1.AF204675"
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3927..4062,4153..4274,4362..4724,4801..4930,5029..5105,
5183..5296,5446..5500,5755..5857))
/gene="At2g41880"
complement(join(3460..3541,3637..3727,3807..3852,
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PSHFGRFSVSHTRSPRSMENDGVHYHFDKRVKEIKDQKFLFASVHNLGTSL
ESVAVAVDSGRCLDIDVOGARSVASSLDALPIFVCPSPMKLELDRLRARGETES
QIQRLRNNAEAEIKEGISSGIFGLIYNDMLECYKKLKNLGLDGLAHVNGVIEGI
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7600..9670
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/db_xref="GI:20196896"
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ATLPPEPFRGFRSPRSATTMSGSEFTTISRFINLVLAGSSMENNELTRVYTOR
EDERQDELMRHEDTDHEBETNPALVDPDQPSGLDPSGDSNGQSGVSTQVRVKA
EYVAKITAMOTAKLAKINRFRKEDAVINMFEOYVKAISMKKIERKLEBRKAKA
MEKQNNVAKORAKAEERBATYAEKRGTEVAKVVEVAVNLMLALGRPAKRSPFSFS"
complement(8642..8664)
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10750..12890
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/note="synonym: T1A7.4"
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12044..12327,12415..12645,12735..12890)
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VEINRQMPREHNTVITLKETTYEDDAVYHLMELCSGELFDRIVARGHTERRAASVYIK
TIIIEVQVCHRGHWARDIKENLFPANKSTASLKADFLSVFFKRGSEFNIVGS
PYVPAVLRVRSYQEDIDMSAGVILVILCGVPPFAETSHGVAKALKSVIDPFRK
PWPVADNNAKOLIKMLIPDRRLTAQOVDHMIQNGKASNVLSGELVYARLKKP
SVNKLKRALRVIAEHLSEVETSCIERFQVMDTSRGKTTIELGIGLOKQIVP
ODDIOILMDGDVDDVDVNEFEVLSVHRIKGNBHLKKATLPPKXNSGYIET
ELRDLADVDVDTSEVVEVALIIVDNRNKGKISYDEPATTMTKTGTMRKASROYSRD
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complement(14694..14717)
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16477..18618

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CDS		join(<16477..16731,16930..16961,17046..17216,17458..17665,17823..17904,17999..18107,18206..18319,18409..>.18618)	
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		/db_xref="GI:2335094"	
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		Cereas:17415"	
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gene		24083..30105	
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		/note="synonym: T1IA7_7; predicted by genSCAN; similar to GP 2191175 AF002720"	
mRNA		join(<24083..24229,24605..24679,24862..24986,25189..25303,25475..25558,25660..25707,25758..25871,26076..26241,26613..26905,27234..27749,27973..28122,28266..28341,28853..28680,28855..29049,29166..29303,29391..29501,29600..29839,29941..30105)>	
CDS		/gene="At2g941830"	
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Query Match	82.5%; Score 19.8; DB 8; Length 91071;
Best Local Similarity	91.3%; Pred. No. 57;
Matches 21; Conservative	0; Mismatches 2; Indels 0; Gaps 0;

Oy	2 AGCCACCAGAAGAGCACCAGAAAT 24
Dd	64909 AACCACAAAAGAGGCCAAAT 64887

RESULT 11	813 bp DNA linear STS 31-MAY-2003
BV071807	S212P676PF6.T0 CZECHIT/EI Mus musculus STS genomic sequence
LOCUS	
DEFINITION	tagged site.

ACCESSION	BV071807
VERSION	BV071807.1 GI:31187602
KEYWORDS	STS.
SOURCE	Mus musculus Mus musculus (house mouse)
ORGANISM	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 813) Wade,C.M., Kulbokas,E.J. III, Kirby,A.W., Zody,M.C., Mullikin,J.C., Lander,E.S., Lindblad-Toh,K. and Daly,M.J. The mosaic structure of variation in the laboratory mouse genome Nature 420 (6915), 574-578 (2002)
TITLE	Nature 420 (6915), 574-578 (2002)
JOURNAL	22354684
MEDLINE	12466852
PUBMED	
COMMENT	Contact: Kerstin Lindblad-Toh Whitehead Institute for Biomedical Research, Center for Genome Research 320 Charles Street, Cambridge, MA 02141, USA Tel: 6172521477 Fax: 6172580903 Email: Kersli@genome.wi.mit.edu Primer A: None Primer B: None STS size: 813 Protocol: WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SvimJ, C3H/HsdJ, and Balb/cByJ. The WGS reads were placed uniquely on the MGCv3 C57BL/6J assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were annotated as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%. Location/Qualifiers 1..813 /organism="Mus musculus" /mol_type="genomic DNA" /strain="CZECHIT/EI" /db_xref="taxon:10090" /map=" + 8 26-777 5648606-5649357" /clone_id="CZECHIT/EI" <1..>813
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ORIGIN	
STS	
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Best Local Similarity	95.2%; Pred. No. 80;
Matches	20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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RESULT 12	
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DEFINITION	Mus musculus chromosome UNK clone RP24-279K10, WORKING DRAFT
ACCESSION	AC134552
VERSION	AC134552
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULFILLTOP.
SOURCE	Mus musculus (house mouse)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1 (bases 1 to 173763) McPherson,J.D. and Waterston,R.H. The sequence of Mus musculus clone 2 (bases 1 to 173763) McPherson,J.D. and Waterston,R.H. Direct Submission
AUTHORS	
JOURNAL	
REFERENCE	
AUTHORS	
TITLE	

JOURNAL Submitted (27-SEP-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 3 (bases 1 to 173763)

AUTHORS McPherson,J.D. and Waterston,R.H.

TITLE Direct Submission

JOURNAL Submitted (20-MAR-2003) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

COMMENT On Mar 20, 2003 this sequence version replaced gi:29124268.

----- Genome Center -----

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc/index.shtml>

Contact: submissions@watson.wustl.edu

Project Information -----

Center project name: M_BB0279K10

----- Summary Statistics -----

Sequencing vector: M13; 0%

Chemistry: Dye-primer ET; 0% of reads

Chemistry: Dye-terminator Big_Dye; 100% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 172608 bases at least Q40

Consensus quality: 173012 bases at least Q30

Consensus quality: 173235 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2809: contig of 2809 bp in length

* 2810 2909: gap of unknown length

* 2910 26146: contig of 2337 bp in length

* 26147 26246: gap of unknown length

* 26247 89830: contig of 63584 bp in length

* 89831 89930: gap of unknown length

* 89931 173763: contig of 83833 bp in length.

FEATURES

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1. 173763

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2910. 26146

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ORIGIN

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Best Local Similarity 95.2%; Pred. No. 93;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGACCCAG 21

DB 91787 CAGCCAGCAAGAGACCCAG 91807

RESULT 13

AC087416 183349 bp DNA linear ROD 15-NOV-2002

LOCUS AC087416

DEFINITION Mus musculus chromosome 2 clone rp23-224116 strain C57BL/6J, complete sequence.

ACCESSION AC087416 GI:25013342

VERSION AC087416.18

KEYWORDS HMG.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 183349)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE 1 (bases 1 to 183349)

JOURNAL Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Mus musculus BAC Clone rp23-224116

REFERENCE 2 (bases 1 to 183349)

AUTHORS Unpublished

TITLE Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

JOURNAL Submitted (10-JUN-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 3 (bases 1 to 183349)

AUTHORS Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (10-JUL-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 4 (bases 1 to 183349)

AUTHORS Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (12-JUL-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 5 (bases 1 to 183349)

AUTHORS Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-2001) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 6 (bases 1 to 183349)

AUTHORS Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (29-JUL-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 7 (bases 1 to 183349)

AUTHORS Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (01-AUG-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

REFERENCE 8 (bases 1 to 183349)

AUTHORS Kim,J., Shauli,S., Yao,Z. and Roe,B.A.

TITLE Direct Submission

JOURNAL Submitted (15-NOV-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA

COMMENT On Nov 15, 2002 this sequence version replaced gi:22002184.

----- Genome Center -----

Center: Department Of Chemistry And Biochemistry

The University Of Oklahoma

Center code:UOKNOR

FEATURES

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Best Local Similarity 95.2%; Pred. No. 93;

Matches 20; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION	Mouse DNA sequence from clone RP23-191L7 on chromosome 2, complete sequence.			
ACCESSION	AL805918			
VERSION	AL805918.5	GI:23395461		
KEYWORDS	HTG.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1 (bases 1 to 213625)			
AUTHORS	Leonagorriert, D.			
TITLE	Direct Submission			
JOURNAL	Submitted (04-OCT-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 1, 2002 this sequence version replaced GI:23337476.			
COMMENT	----- Genome Center ----- Center: Wellcome Trust Sanger Institute Center code: SC Web file: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk -----			
	<p>During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.</p> <p>This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPOT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-191L7 is from the RPCI-23 Mouse PAC library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/backpac/home.htm</p> <p>VECTOR: pBACe3.6.</p>			
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Best Local Similarity	95.2%	Pred. No. 93;		
Misc Match	20;	Conservative	0;	Mismatches
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Db	136743	AGCCACCAAGAGAGACTCACA	136763	

LOCUS VCCYNA 1603 bp mRNA linear PLN 03-OCT-1994
 DEFINITION v carnunculus mRNA for cynarase.
 ACCESSION X69193
 VERSION X69193.1 GI:499015
 KEYWORDS aspartic proteinase; cynarase.
 SOURCE Cynara cardunculus
 ORGANISM Cynara cardunculus
 Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Cardioideae;
 Cardueae; Cynara.
 REFERENCE 1 (bases 1 to 1600)
 AUTHORS Cordeiro,M.C., Xue,Z.T., Pietrzak,M., Pais,M.S. and Brodelius,P.E.
 TITLE Isolation and characterization of a cDNA from flowers of Cynara
 cardunculus encoding cyprosin (an aspartic proteinase) and its use
 to study the organ-specific expression of cyprosin
 JOURNAL Plant Mol. Biol. 24 (5), 733-741 (1994)
 MEDLINE 94250836
 PUBMED 8193298
 2 (bases 1 to 1600)
 AUTHORS Brodelius,P.
 TITLE Direct Submission
 REFERENCE Submitted (13-NOV-1992) P. Brodelius, University of Lund, Dept of
 Plant Biochemistry, POB 7007, 220 07 Lund, SWEDEN
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 Best Local Similarity 87.5%; Pred. NO. 1e+02;
 Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CAGCCACCAAGAGAGCCAGAT 24
 ||||| ||||| ||||| |||||
 DB 792 CAGCCACCAAGAGAGCTCCAGAT 769

Miss Margaret (Mrs. J. J.)

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: July 30, 2004, 20:19:46 ; Search time 70 Seconds
(without alignments)
190.269 Million cell updates/sec

Title: US-09-831-272-7

Perfect score: 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	19	79.2	3692	2	US-08-588-983-17	Sequence 17, Appl
2	19	79.2	3692	2	US-08-588-976-17	Sequence 17, Appl
3	17.4	72.5	2606	2	US-08-701-233B-11	Sequence 11, Appl
4	16.6	69.2	289	4	US-09-443-184-111	Sequence 111, Appl
5	16.6	69.2	349	4	US-09-833-181-1287	Sequence 1287, Appl
6	16.6	69.2	2543	4	US-09-976-594-575	Sequence 575, Appl
7	16.6	69.2	2636	4	US-09-976-594-383	Sequence 383, Appl
8	16.2	67.5	375	4	US-09-702-705-961	Sequence 961, Appl
9	16.2	67.5	375	4	US-09-702-705-1158	Sequence 1158, Appl
10	16.2	67.5	375	4	US-09-736-457-961	Sequence 961, Appl
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18	16.2	67.5	571	4	US-09-614-124B-921	Sequence 921, Appl
19	16.2	67.5	791	4	US-09-671-325-921	Sequence 921, Appl
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24	16.2	67.5	20084	3	US-08-943-731-5	Sequence 89, Appl
25	16.2	67.5	20084	3	US-08-943-731-5	Sequence 89, Appl
26	16.2	67.5	20084	3	US-08-943-731-5	Sequence 89, Appl
27	16.2	67.5	20084	3	US-08-943-731-5	Sequence 89, Appl

28	16	66.7	3839	4	US-09-245-248B-54	Sequence 54, Appl
29	16	66.7	29485	4	US-09-785-381-6	Sequence 6, Appl
30	15.8	65.8	109	2	US-08-427-097-8	Sequence 8, Appl
31	15.8	65.8	109	2	US-08-878-957-8	Sequence 8, Appl
32	15.8	65.8	399	4	US-09-188-930-63	Sequence 63, Appl
33	15.8	65.8	399	4	US-09-312-283C-63	Sequence 63, Appl
34	15.8	65.8	1695	2	US-08-878-957-31	Sequence 31, Appl
35	15.8	65.8	1746	2	US-08-878-957-29	Sequence 29, Appl
36	15.8	65.8	1746	2	US-08-878-957-29	Sequence 29, Appl
37	15.8	65.8	1752	1	US-08-427-097-13	Sequence 13, Appl
38	15.8	65.8	1752	1	US-08-427-097-13	Sequence 13, Appl
39	15.8	65.8	1752	1	US-08-427-097-13	Sequence 13, Appl
40	15.8	65.8	1752	2	US-08-878-957-13	Sequence 13, Appl
41	15.8	65.8	1752	2	US-08-878-957-13	Sequence 13, Appl
42	15.8	65.8	1752	2	US-08-878-957-13	Sequence 13, Appl
43	15.8	65.8	9103	1	US-08-466-033-182	Sequence 182, Appl
44	15.8	65.8	9103	1	US-08-444-733-182	Sequence 182, Appl
45	15.8	65.8	9103	2	US-08-464-134-182	Sequence 182, Appl

ALIGNMENTS

RESULT 1
US-08-588-983-17/c
Sequence 17, Application US/08588983
Patent No. 5854067
GENERAL INFORMATION:
APPLICANT: Christopher B. Newgard, et al.
TITLE OF INVENTION: Methods and Compositions
TITLE OF INVENTION: for Inhibiting Hexokinase
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSER: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,983
FILING DATE: Concurrently herewith
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Fusey, Shelley P.M.
REGISTRATION NUMBER: 39,458
REFERENCE/DOCKET NUMBER: UTSD:424/FUS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: n/a
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 3692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-588-983-17

Query Match 79.2%; Score 19; DB 2; Length 3692;
Best Local Similarity 100.0%; Pred. No. 12;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGGACCC 19
Db 1087 CAGCCACCAAGAGGACCC 1069

RESULT 2

US-08-588-976-17/C

Sequence 17, Application US/08588976

Patent No. 5891717

GENERAL INFORMATION:

APPLICANT: Christopher B. Newgard, et al.

TITLE OF INVENTION: Methods and Compositions for

TITLE OF INVENTION: Inhibiting Hexokinase

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSER: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: US

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/588,976

FILING DATE: Concurrently herewith

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Fusey, Shelley P.M.

REGISTRATION NUMBER: 39,458

REFERENCE/DOCKET NUMBER: UTSD:481/FUS

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: n/a

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:

LENGTH: 3692 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-588-976-17

Query Match 79.2%; Score 19; DB 2; Length 3692;

Best Local Similarity 100.0%; Pred. No. 12;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19

Db 1087 CAGCCACCAAGAGAGACC 1069

RESULT 3

US-08-701-233B-1/C

Sequence 1, Application US/08701233B

Patent No. 5861308

GENERAL INFORMATION:

APPLICANT: Pfreundschuh, Michael; Renner, Christoph

TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ASSOCIATED WITH T CELL

TITLE OF INVENTION: ACTIVATION AND USES THEREOF

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSER: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/701,233B

FILING DATE: 21-August-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, NO. 5861308man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5440

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2606 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-701-233B-1

Query Match 72.5%; Score 17.4; DB 2; Length 2606;

Best Local Similarity 94.7%; Pred. No. 63;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCACCAAGAGAGACCAGA 22

Db 1917 CCACCAAGAGAGACCCTGA 1899

RESULT 4

US-09-443-184-111/C

Sequence 111, Application US/09443184A

Patent No. 6372431

GENERAL INFORMATION:

APPLICANT: Cunningham, Mary Jane

APPLICANT: Zweigler, Gary

APPLICANT: Kaser, Matthew R.

APPLICANT: Panzer, Scott

APPLICANT: Selhammer, Jeffrey J.

APPLICANT: Yue, Henry

APPLICANT: Baughn, Mariah

APPLICANT: Azimzai, Valda

APPLICANT: Lal, Preeti

TITLE OF INVENTION: MAMMALIAN TOXICOLOGICAL RESPONSE MARKERS

FILE REFERENCE: PC-0007 US

CURRENT APPLICATION NUMBER: US/09/443,184A

CURRENT FILING DATE: 1999-11-19

NUMBER OF SEQ ID NOS: 138

SOFTWARE: PERL Program

SEQ ID NO 111

LENGTH: 289

TYPE: DNA

ORGANISM: Rattus norvegicus

FEATURES:

NAME/KEY: misc feature

OTHER INFORMATION: Inocyte ID NO. 6372431 700067537H1

US-09-443-184-111

Query Match 69.2%; Score 16.6; DB 4; Length 289;

Best Local Similarity 82.6%; Pred. No. 1.1e+02;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACCAGA 23

Db 267 CAGCCACCAAGAGAGATCCAGCA 245

RESULT 5

US-09-833-381-1287/C

Sequence 1287, Application US/09833381

Patent No. 6672186

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: NO. 6672186el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

```

; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1287
; LENGTH: 349
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(349)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-381-1287
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```
Query Match          69.2%; Score 16.6; DB 4; Length 349;
Best Local Similarity 82.6%; Pred. No. 1.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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```
QY 1 CAGCCACCAAGAGAGCCAGAA 23
Db 45 CAGACACCAAGAGAGCCAGTA 23
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```

RESULT 6
US-09-976-594-575/c
; Sequence 575, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 575
; LENGTH: 2543
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1859458C81
US-09-976-594-575
```

```
Query Match          69.2%; Score 16.6; DB 4; Length 2543;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 CAGCCACCAAGAGAGCCAGAA 23
Db 2081 CAGACACCAAGAGAGCCAGTA 2059
```

```

RESULT 7
US-09-976-594-383
; Sequence 383, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 383
; LENGTH: 2636
```

```

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 238026.4
US-09-976-594-383
```

```
Query Match          69.2%; Score 16.6; DB 4; Length 2636;
Best Local Similarity 82.6%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY 1 CAGCCACCAAGAGAGCCAGAA 23
Db 906 CAGCAGCCCAAGAGGCCCCAGAA 928
```

```

RESULT 8
US-09-702-705-961/c
; Sequence 961, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 961
; LENGTH: 375
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-702-705-961
```

```
Query Match          67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 AGCCACCAAGAGAGCCAGAA 22
Db 163 AGCCACCAAGAGAGCCAGAA 143
```

```

RESULT 9
US-09-702-705-1158
; Sequence 1158, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
```

SEQ ID NO 1158
LENGTH: 375
TYPE: DNA
ORGANISM: Homo sapien
US-09-702-705-1158

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
DB 213 AGCCACCAAGAGAGACCAGA 233

RESULT 10
US-09-736-457-961/C
Sequence 961, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 961
LENGTH: 375
TYPE: DNA
ORGANISM: Homo sapien
US-09-736-457-961

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
DB 163 AGCCACCAAGAGAGACCAGA 143

RESULT 11
US-09-736-457-1158
Sequence 1158, Application US/09736457
Patent No. 6509448
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1158
LENGTH: 375
TYPE: DNA
ORGANISM: Homo sapien
US-09-736-457-1158

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
DB 213 AGCCACCAAGAGAGACCAGA 233

RESULT 12
US-09-614-124B-961/C
Sequence 961, Application US/09614124B
Patent No. 6630574
GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 961
LENGTH: 375
TYPE: DNA
ORGANISM: Homo sapien
US-09-614-124B-961

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
DB 163 AGCCACCAAGAGAGACCAGA 143

RESULT 13
US-09-614-124B-1158
Sequence 1158, Application US/09614124B
Patent No. 6630574
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
FILE REFERENCE: 210121.478C9
CURRENT APPLICATION NUMBER: US/09/614,124B
CURRENT FILING DATE: 2001-07-11
NUMBER OF SEQ ID NOS: 1668
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1158
LENGTH: 375

TYPE: DNA
ORGANISM: Homo sapien
US-09-614-124B-1158

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
Db 213 AGCCACCAAGAGAGACCAGA 233

RESULT 14
US-09-671-325-961/c
Sequence 961, Application US/09671325
Patent No. 6667154

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.

APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick

APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12

CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 1825

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 961

LENGTH: 375

TYPE: DNA

ORGANISM: Homo sapien

US-09-671-325-961

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
Db 163 AGCCACCAAGAGAGACCAGA 143

RESULT 15
US-09-671-325-1158
Sequence 1158, Application US/09671325
Patent No. 6667154

GENERAL INFORMATION:

APPLICANT: Wang, Tonglong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.

APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darrick

APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane

APPLICANT: Fan, Liqun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.478C12

CURRENT APPLICATION NUMBER: US/09/671,325

CURRENT FILING DATE: 2000-09-26

NUMBER OF SEQ ID NOS: 1825

SOFTWARE: FaastSeq for Windows Version 3.0

SEQ ID NO 1158

LENGTH: 375

TYPE: DNA

ORGANISM: Homo sapien
US-09-671-325-1158

Query Match 67.5%; Score 16.2; DB 4; Length 375;
Best Local Similarity 85.7%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGACCAGA 22
|||||
Db 213 AGCCACCAAGAGAGACCAGA 233

Search completed: July 30, 2004, 22:06:01
JOD time : 72 secs

It's "Big Black" (uspo)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 30, 2004, 20:26:46 ; Search time 406 Seconds
(without alignments)
289.841 Million cell updates/sec

Title: US-09-831-272-7

Perfect score: 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA.*
1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
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5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/prodata/2/pubpna/US10_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19.8	82.5	431	US-09-770-423-146	Sequence 146, App
C 2	19.8	82.5	1451	US-10-424-599-65132	Sequence 65132, A
C 3	19.8	82.5	2868	US-09-938-842A-496	Sequence 496, App
C 4	19.8	82.5	2868	US-09-938-842A-496	Sequence 496, App
C 5	19.8	82.5	141	US-10-350-923B-45	Sequence 45, App
C 6	19.8	79.2	3062	US-09-880-107-3382	Sequence 3382, App
C 7	19.8	79.2	3062	US-10-942-887-728	Sequence 728, App
C 8	19.8	79.2	3062	US-10-172-118-728	Sequence 728, App
C 9	19.8	79.2	3062	US-10-172-118-728	Sequence 728, App
C 10	19.8	79.2	3205	US-10-177-809-1	Sequence 214, App
C 11	19.8	79.2	3205	US-10-177-809-1	Sequence 1, Appl
C 12	19.8	79.2	3205	US-10-177-809-3	Sequence 3, Appl
C 13	19.8	79.2	3692	US-10-152-319A-1767	Sequence 1767, App
C 14	19.8	79.2	3692	US-10-152-319A-1767	Sequence 1767, App
C 14	19.8	79.2	3692	US-10-191-803-138	Sequence 138, App

C 15	19	79.2	18772	10	US-09-764-861-63	Sequence 63, Appl
C 16	19	79.2	18772	13	US-09-764-861-63	Sequence 63, Appl
C 17	19	79.2	18772	15	US-10-115-928-63	Sequence 63, Appl
C 18	19	79.2	18772	15	US-10-115-928-63	Sequence 63, Appl
C 19	18.2	75.8	625	13	US-10-027-632-211873	Sequence 211873, A
C 20	18.2	75.8	625	13	US-10-027-632-211873	Sequence 211873, A
C 21	18.2	75.8	625	16	US-10-027-632-211874	Sequence 211874, A
C 22	18.2	75.8	625	16	US-10-027-632-211874	Sequence 211874, A
C 23	18.2	75.8	625	16	US-10-027-632-211874	Sequence 211874, A
C 24	18.2	75.8	625	16	US-10-027-632-211874	Sequence 211874, A
C 25	17.8	74.2	41	12	US-10-035-833A-123	Sequence 123, App
C 26	17.8	74.2	41	12	US-10-035-833A-123	Sequence 123, App
C 27	17.8	74.2	41	12	US-10-035-833A-123	Sequence 123, App
C 28	17.8	74.2	41	12	US-10-035-833A-123	Sequence 123, App
C 29	17.8	74.2	41	12	US-10-035-833A-123	Sequence 123, App
C 30	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 31	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 32	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 33	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 34	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 35	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 36	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 37	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 38	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 39	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 40	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 41	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 42	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 43	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 44	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl
C 45	17.6	73.3	529	13	US-10-236-392-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-770-423-146/C
Sequence 146, Application US/09770423
Publication No. US20020040490A1
GENERAL INFORMATION:
APPLICANT: Gorlach, Jörn
APPLICANT: An, Yong-Qiang
APPLICANT: Hamilton, Carol M.
APPLICANT: Price, Jennifer L.
APPLICANT: Raines, Tracy M.
APPLICANT: Yu, Yang
APPLICANT: Rameaka, Joshua G.
APPLICANT: Page, Amy
APPLICANT: Mathew, Abraham V.
APPLICANT: Ledford, Brooke L.
APPLICANT: Moessner, Jeffrey P.
APPLICANT: Haas, William David
APPLICANT: Garcia, Carlos A.
APPLICANT: Krickler, Maja
APPLICANT: Slader, Ted
APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
FILE REFERENCE: 2028 (PARA-01/PRV)
CURRENT FILING DATE: 2001-01-26
PRIORITY FILING DATE: 2000-01-27
PRIORITY FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 146
LENGTH: 431
TYPE: DNA
ORGANISM: Arabidopsis thaliana

US-09-770-423-146

Query Match 82.5%; Score 19.8; DB 13; Length 431;
Best Local Similarity 91.3%; Pred. No. 38;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGCCCAAGAT 24
DB 367 AACCAACCAAGAGAGCCCAAGAT 345

RESULT 2
US-10-424-599-65132
Sequence 65132, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 65132
LENGTH: 1451
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_29827C.1
US-10-424-599-65132

Query Match 82.5%; Score 19.8; DB 13; Length 1451;
Best Local Similarity 91.3%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGCCCAAGAT 24
DB 427 AACCAACCAAGAGAGCCCAAGAT 449

RESULT 3
US-09-938-842A-496/C
Sequence 496, Application US/09938842A
Publication No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: S01300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 496
LENGTH: 2868
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-496

Query Match 82.5%; Score 19.8; DB 9; Length 2868;
Best Local Similarity 91.3%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGCCCAAGAT 24
DB 694 AACCAACCAAGAGAGCCCAAGAT 672

RESULT 4
US-09-938-842A-496/C
Sequence 496, Application US/09938842A
Publication No. US2004009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: S01300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 496
LENGTH: 2868
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-496

Query Match 82.5%; Score 19.8; DB 11; Length 2868;
Best Local Similarity 91.3%; Pred. No. 37;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AGCCACCAAGAGAGCCCAAGAT 24
DB 694 AACCAACCAAGAGAGCCCAAGAT 672

RESULT 5
US-10-350-923B-45/C
Sequence 45, Application US/10350923B
Publication No. US2004002084A1
GENERAL INFORMATION:
APPLICANT: Dotson, Stanton B.
APPLICANT: Ma, Xiao Jun
TITLE OF INVENTION: Nucleic acid, polypeptides, vectors, and cells derived from activ
TITLE OF INVENTION: eosinophil cells
FILE REFERENCE: S0157-01
CURRENT APPLICATION NUMBER: US/10/350,923B
CURRENT FILING DATE: 2003-01-24
PRIOR APPLICATION NUMBER: US/09/454,280
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: PCT/US99/28773
PRIOR FILING DATE: 1999-06-12
PRIOR APPLICATION NUMBER: US 60/111,006
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 141
TYPE: DNA
ORGANISM: Homo sapiens
US-10-350-923B-45

Query Match 79.2%; Score 19; DB 16; Length 141;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGAGCC 19

Db 102 CAGCCACCAAGAGACC 84

RESULT 6
US-09-880-107-3382/c
; Sequence 3382, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schert, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-MO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3382
; LENGTH: 3062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U51333
US-09-880-107-3382

Query Match 79.2%; Score 19; DB 9; Length 3062;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGACC 19
Db 1081 CAGCCACCAAGAGACC 1063

RESULT 7
US-10-342-887-728/c
; Sequence 728, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 68/238,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 728
; LENGTH: 3062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-728

Query Match 79.2%; Score 19; DB 13; Length 3062;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGACC 19
Db 1081 CAGCCACCAAGAGACC 1063

RESULT 8
US-10-172-118-728/c
; Sequence 728, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 728
; LENGTH: 3062
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 002115
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-728

Query Match 79.2%; Score 19; DB 13; Length 3062;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGACC 19
Db 1081 CAGCCACCAAGAGACC 1063

RESULT 9
US-10-717-597-214/c
; Sequence 214, Application US/10717597
; Publication No. US20040110221A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael E.
; APPLICANT: Twine, Natalie C.
; APPLICANT: Dornier, Andrew J.
; APPLICANT: Trepicchio, William L.
; APPLICANT: Stonim, Donna K.
; APPLICANT: Scover, Jennifer A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
; FILE REFERENCE: AM101080L
; CURRENT APPLICATION NUMBER: US/10/717,597
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 60/459,782
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 60/427,982
; PRIOR FILING DATE: 2002-11-21
; NUMBER OF SEQ ID NOS: 4904
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214
; LENGTH: 3062
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-717-597-214

Query Match 79.2%; Score 19; DB 17; Length 3062;

Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 10
US-10-177-809-1/c

/ Sequence 1, Application US/10177809
/ Publication No. US20030148305A1
/ GENERAL INFORMATION:
/ APPLICANT: Grosse, William M.,
/ APPLICANT: Alsobrook, John P.,
/ APPLICANT: Lepley, Denise M.,
/ APPLICANT: Burgess, Catherine E.,
/ APPLICANT: Bader, Joel S.,
/ APPLICANT: Banaal, Aruna,
/ APPLICANT: Pena, Carol E.A.,
/ APPLICANT: Shinkets, Richard A.,
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Anderson, David
/ APPLICANT: Zhong, Mei
/ APPLICANT: Miller, Charles
/ APPLICANT: Vernet, Corine
/ APPLICANT: Hjalte, Tord
/ TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, SINGLE NUCLEOTIDE POLYMORPHISMS AND
/ FILE REFERENCE: 21402-390
/ CURRENT APPLICATION NUMBER: US/10/177,809
/ PRIOR FILING DATE: 2003-01-28
/ PRIOR APPLICATION NUMBER: 60/311,285
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 60/299,949
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/300,290
/ PRIOR FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: 60/302,883
/ PRIOR FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: 60/327,345
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 60/327,467
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 60/327,892
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/354,586
/ PRIOR FILING DATE: 2002-02-05
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Custom
/ SEQ ID NO 1
/ LENGTH: 3205
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (75)..(1164)
US-10-177-809-1

Query Match 79.2%; Score 19; DB 15; Length 3205;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 11
US-10-177-809-3/c
/ Sequence 3, Application US/10177809

/ Publication No. US20030148305A1
/ GENERAL INFORMATION:
/ APPLICANT: Grosse, William M.,
/ APPLICANT: Alsobrook, John P.,
/ APPLICANT: Lepley, Denise M.,
/ APPLICANT: Burgess, Catherine E.,
/ APPLICANT: Bader, Joel S.,
/ APPLICANT: Banaal, Aruna,
/ APPLICANT: Pena, Carol E.A.,
/ APPLICANT: Shinkets, Richard A.,
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Anderson, David
/ APPLICANT: Zhong, Mei
/ APPLICANT: Miller, Charles
/ APPLICANT: Vernet, Corine
/ APPLICANT: Hjalte, Tord
/ TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, SINGLE NUCLEOTIDE POLYMORPHISMS AND
/ FILE REFERENCE: 21402-390
/ CURRENT APPLICATION NUMBER: US/10/177,809
/ PRIOR FILING DATE: 2003-01-28
/ PRIOR APPLICATION NUMBER: 60/311,285
/ PRIOR FILING DATE: 2001-08-09
/ PRIOR APPLICATION NUMBER: 60/299,949
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/300,290
/ PRIOR FILING DATE: 2001-06-22
/ PRIOR APPLICATION NUMBER: 60/302,883
/ PRIOR FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: 60/327,345
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 60/327,467
/ PRIOR FILING DATE: 2001-10-05
/ PRIOR APPLICATION NUMBER: 60/327,892
/ PRIOR FILING DATE: 2001-10-09
/ PRIOR APPLICATION NUMBER: 60/354,586
/ PRIOR FILING DATE: 2002-02-05
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Custom
/ SEQ ID NO 3
/ LENGTH: 3205
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-177-809-3

Query Match 79.2%; Score 19; DB 15; Length 3205;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 12
US-10-177-809-5/c
/ Sequence 5, Application US/10177809
/ Publication No. US20030148305A1
/ GENERAL INFORMATION:
/ APPLICANT: Grosse, William M.,
/ APPLICANT: Alsobrook, John P.,
/ APPLICANT: Lepley, Denise M.,
/ APPLICANT: Burgess, Catherine E.,
/ APPLICANT: Bader, Joel S.,
/ APPLICANT: Banaal, Aruna,
/ APPLICANT: Pena, Carol E.A.,
/ APPLICANT: Shinkets, Richard A.,
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Zernusen, Bryan
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Anderson, David

APPLICANT: Zhong, Mei
APPLICANT: Miller, Charles
APPLICANT: Vermet, Corine
APPLICANT: Hjalte, Tor
TITLE OF INVENTION: NUCLEIC ACIDS, POLYPEPTIDES, SINGLE NUCLEOTIDE POLYMORPHISMS AND
FILE REFERENCE: 21402-390
CURRENT APPLICATION NUMBER: US/10/177,809
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/311,285
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/299,949
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/300,290
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/302,883
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/327,345
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,467
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,892
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/354,586
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Custom
SEQ ID NO 5
LENGTH: 3205
TYPE: DNA
ORGANISM: Homo sapiens
US-10-177-809-5

Query Match 79.2%; Score 19; DB 15; Length 3205;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1081 CAGCCACCAAGAGAGACC 1063

RESULT 13
US-10-152-319A-1767/c
Sequence 1767, Application US/10152319A
Publication No. US20040072160A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,810
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,807
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/303,808
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR FILING DATE: 2001-08-28
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR FILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILING DATE: 2001-10-22
Remaining Prior Application data removed - See file Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1767
LENGTH: 3692
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. NM_022179
US-10-152-319A-1767

Query Match 79.2%; Score 19; DB 12; Length 3692;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1087 CAGCCACCAAGAGAGACC 1069

RESULT 14
US-10-191-803-138/c
Sequence 138, Application US/10191803
Publication No. US20040014040A1
GENERAL INFORMATION:
APPLICANT: MENDRICK, Donna
APPLICANT: PORTER, Mark
APPLICANT: JOHNSON, Kory
APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/377,611
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 1140
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 138
LENGTH: 3692
TYPE: DNA
ORGANISM: Rattus norvegicus
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_022179
US-10-191-803-138

Query Match 79.2%; Score 19; DB 16; Length 3692;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACC 19
DB 1087 CAGCCACCAAGAGAGACC 1069

RESULT 15
US-09-764-861-63/c
Sequence 63, Application US/09764861
Publication No. US20030171252A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

```

; FILE REFERENCE: PT204
; CURRENT APPLICATION NUMBER: US/09/764,861
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 63
; LENGTH: 18772
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9782)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-861-63

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Query Match          79.2%; Score 19; DB 10; Length 18772;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 CAGCCACCAAGAGAGGCC 19
Db      708 CAGCCACCAAGAGAGGCC 690

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Search completed: July 30, 2004, 22:13:04
 Job time : 410 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2004, 20:13:41 ; Search time 2963 Seconds
(without alignments)
241.881 Million cell updates/sec

Title: US-09-831-272-7
Perfect score: 24
Sequence: 1 cagccaccaagagagaccagat 24

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_escba:*
2: em_escbm:*
3: em_escin:*
4: em_escnu:*
5: em_escov:*
6: em_escpl:*
7: em_escro:*
8: em_escst:*
9: gb_esc1:*
10: gb_esc2:*
11: gb_esc3:*
12: gb_esc4:*
13: gb_esc5:*
14: gb_esc6:*
15: em_escfun:*
16: em_escgm:*
17: em_escgm:*
18: em_escgm:*
19: em_escgm:*
20: em_escgm:*
21: em_escgm:*
22: em_escgm:*
23: em_escgm:*
24: em_escgm:*
25: em_escgm:*
26: em_escgm:*
27: em_escgm:*
28: gb_esc1:*
29: gb_esc2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20.4	85.0	934	14	CK269862 EST715940
2	19.8	82.5	347	29	CC468543 CH240.139
3	19.8	82.5	528	9	AV529210 AV529210
4	19.8	82.5	531	28	AZ114521 RPT-23-4

C 5	19.8	82.5	534	9	AV529714
C 6	19.8	82.5	705	14	CK317567
C 7	19.8	82.5	1076	10	EG024130
C 8	19.8	82.5	1082	10	BE729686
C 9	19.2	80.0	242	9	AV271379
C 10	19.2	80.0	257	9	AV333896
C 11	19.2	80.0	708	13	BU026771
C 12	19.2	80.0	728	28	AZ312990
C 13	19.2	80.0	899	29	CC518089
C 14	19.2	80.0	359	10	CC518089
C 15	19.2	80.0	359	10	BF901013
C 16	18.8	78.3	321	14	CB972921
C 17	18.8	78.3	385	14	CB702933
C 18	18.8	78.3	452	14	CD802324
C 19	18.8	78.3	463	10	BF427213
C 20	18.8	78.3	466	13	BQ798315
C 21	18.8	78.3	506	10	AW140945
C 22	18.8	78.3	510	12	BG813094
C 23	18.8	78.3	550	9	AA990846
C 24	18.8	78.3	562	10	AM913869
C 25	18.8	78.3	566	28	AQ962724
C 26	18.8	78.3	591	14	CF413809
C 27	18.8	78.3	622	14	CA352741
C 28	18.8	78.3	635	10	BB625968
C 29	18.8	78.3	643	13	BQ208827
C 30	18.8	78.3	653	13	BQ193103
C 31	18.8	78.3	656	10	BF270340
C 32	18.8	78.3	669	28	AQ962725
C 33	18.8	78.3	670	13	BQ799382
C 34	18.8	78.3	670	14	CF384461
C 35	18.8	78.3	704	14	CA505029
C 36	18.8	78.3	706	13	BX845101
C 37	18.8	78.3	710	28	CC157138
C 38	18.8	78.3	719	10	BF966746
C 39	18.8	78.3	759	14	CB319952
C 40	18.8	78.3	796	13	BQ799340
C 41	18.8	78.3	830	12	BG518541
C 42	18.8	78.3	832	13	BU428105
C 43	18.8	78.3	845	29	CG820963
C 44	18.8	78.3	892	13	BU910667
C 45	18.8	78.3	913	29	CG054407

ALIGNMENTS

RESULT 1
CK269862/c 934 bp mRNA linear EST 12-DEC-2003
LOCUS EST715940 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION clone POACP48 5' end, mRNA sequence.
ACCESSION CK269862
VERSION CK269862
KEYWORDS EST.
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

REFERENCE 1 (bases 1 to 934)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karanycheva, S.A. and Baker, B.
TITLE Generation of ESTs from abiotic stressed potato tissue
JOURNAL Unpublished (2003)
COMMENT Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-arrays@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1..934
/organism="Solanum tuberosum"
/mol_type="mRNA"

FEATURES

source

/cultivar="Kennebec"
 /db_xref="taxon:4113"
 /clone="POACp48"
 /tissue_type="abiotic stress treated leaf and root tissue"
 /lab_host="DH10B-TonA"
 /clone_id="potato abiotic stress cDNA library"
 /note="Vector: pCMVSPORT6.1, Site 1: EcoRI; Site 2: NotI;
 supplier: Solanum tuberosum var. Kennebec plants were
 grown from cuttings on a 16hr light/8 hr dark cycle at 25
 C for 3-4 weeks. Abiotic stress conditions were applied to
 four separate sets of plants. Set 1 involved saturation of
 the soil with 150 mM NaCl and tissues were harvested at
 following application of the salt stress (leaves: 2hr,
 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
 Set 2 were grown under the standard conditions and then
 were water stressed by withdrawal of further watering
 applications. Drought stressed plants were harvested after
 cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
 and 5d). Set 3 were grown under the standard conditions
 and then were cold stressed by placement at 4 C. Cold
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 and 2d. Set 4 were grown under the standard conditions and
 then were heat stressed by placement at 35 C. Heat
 stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
 2d and 4d and heat-stressed roots were harvested at 6 hr,
 12 hr, 1 d, and 4d. RNA was isolated from all tissues and
 equal RNA from each tissue and stress was pooled to
 construct the cDNA library. RNA sample."

Query Match	85.0%	Score 20.4	DB 14	Length 934
Best Local Similarity	95.5%	Pred. No. 4.8e+02		
Matches 21	Conservative 0	Mismatches 1	Indels 0	Gaps 0

0y	2	AGCCACCAAGAGGCCAGAA	23
Db	171	AGCCACCAAGAGGCCAGAA	150

RESULT 2	CC468543/c	CC468543	347 bp	DNA	linear	GSS 12-JUN-2003
LOCUS	CC468543					
DEFINITION	CH240_139N06.TV CHORI-240 Bos taurus genomic clone CH240_139N06.					
ACCESSION	CC468543					
VERSION	CC468543.1					
KEYWORDS	GSS.					
SOURCE	Bos taurus (cow)					
ORGANISM	Bos taurus					

REFERENCE	1 (bases 1 to 347)
AUTHORS	Coستا,J.N., Mota,M. and Caetano,A.R.
TITLE	Brazil's Contribution to End-Sequencing the Bovine BAC Library
JOURNAL	CHORI-240
COMMENT	Unpublished (2003)
	Other_GSSs: CH240_139N06.TU

JOURNAL
COMMENT

Unpublished (2003)
Other_GSSs: CH240_139N06.TU
Contact: Caetano AR
Department of Biotechnology
Embrapa Recursos Genéticos e Biotecnologia
Parque Estação Biológica, Final Av. W/5 Norte, Brasília-DF C.P.
02372, 70770-900 Brasil
Tel.: 55 61 448 4778
Fax: 55 61 340 3658
Email: acetanoc@cenargen.embrapa.br

Clones are derived from the bovine BAC library CHORI-240
(<http://www.chori.org/bacpac/bovine240.htm>). Bases shown have Phred
quality value equal to or higher than 20. Bases with quality value
below 20 were masked with 'N'. For BAC library availability, please
contact Pieter de Jong (pdejong@mail.chor.org). Clones may be
purchased from BACPAC Resources

(<http://www.chori.org/bacpac/orderinginformation.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by Embrapa Recursos Genéticos e Biotecnologia with financing from Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq), Brazil.

Plates: 139 row: N column: 06

Seq primer: T7

Class: BAC ends

High quality sequence: stop: 347.

Location/Qualifiers

1..347

source

FEATURES	Location/Qualifiers
SOURCE	1. .347

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/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Dreed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_139N06"
/sex="Male"
/cell_type="Blood"
/clone_1fb="CHOR-240"
/notes="vector: PRABAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHOR1-240 bovine BAC
library (male) produced by Pieter de Jong"

```

Query Match	82.5%	Score 19.8	DB 29	Length 347
Best Local Similarity	91.3%	Pred. No. 6.4e+02		
Matches 21	Conservative 0	Mismatches 2	Indels 0	Gaps 0

Qy	2	AGCCACCAAGAGAGCCCGAAT	24
Db	298	AGCCACCAAGAGAGCCCGAAT	276

[illegible]

REFERENCE AUTHORS TITLE
1 (bases 1 to 528) Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S. A large scale analysis of cDNA in <i>Arabidopsis thaliana</i> : Generation

of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)

COMMENT
PUBMED
MEDLINE
20363093
10907847
Contact: Erika Asamizu

Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizuka@kazusa.or.jp, URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES	Location/Qualifiers
source	1. 528

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="AP213007R"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/clone_id="Arabidopsis thaliana aboveground organs two to six-week old"
/note="Vector: pBluescriptRI SK-; Site_1: EcoRI; Site_2: XhoI"

```

ORIGIN

Query Match 82.5%; Score 19.8; DB 9; Length 528;
 Best Local Similarity 91.3%; Pred. No. 7.2e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCCACCAAGAGAGACCCAGAT 24
 |||||
 Db 44 AACCCACCAAGAGAGACCCAGAT 22

RESULT 4
 AZ114521 531 bp DNA linear GSS 12-MAY-2000
 LOCUS RPCI-23-460E1.TV RPCI-23 Mus musculus genomic clone RPCI-23-460E1,
 DEFINITION genomic survey sequence.
 ACCESSION AZ114521
 VERSION AZ114521.1 GI:7774836
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
 1 (bases 1 to 531)
 Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
 Akinel, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de
 Jong, P. and Fraser, C. M.
 Mouse BAC End Sequences from Library RPCI-23
 Unpublished (1999)
 Other_GSSs: RPCI-23-460E1.TV
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.html>)
 or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html
 Plate: 460 row: E column: 1
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..531
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-460E1"
 /sex="Female"
 /lab_host="DH10B"
 /clone_1lb="RPCI-23"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:
 EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI MethyIase. Size
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN
 Query Match 82.5%; Score 19.8; DB 28; Length 531;
 Best Local Similarity 91.3%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCCACCAAGAGAGACCCAGAA 23
 |||||
 Db 150 CAGCCACCAAGAGAGACCCAGAA 172

ORIGIN
 Query Match 82.5%; Score 19.8; DB 28; Length 531;
 Best Local Similarity 91.3%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCCACCAAGAGAGACCCAGAA 23
 |||||
 Db 150 CAGCCACCAAGAGAGACCCAGAA 172

RESULT 5
 AV529714/c 534 bp mRNA linear EST 01-SEP-2000
 LOCUS AV529714 Arabidopsis thaliana aboveground organs two to six-week
 DEFINITION old Arabidopsis thaliana CDNA clone APZ44905' 5', mRNA sequence.
 ACCESSION AV529714
 VERSION AV529714.1 GI:8689997
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 534)
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 A large scale analysis of cDNA in Arabidopsis thaliana: Generation
 of 12,028 non-redundant expressed sequence tags from normalized and
 size-selected cDNA libraries
 DNA Res. 7 (3), 175-180 (2000)
 JOURNAL 2063093
 MEDLINE 10907847
 PUBMED
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp URL: <http://www.kazusa.or.jp/en/plant/>.

FEATURES
 source Location/Qualifiers
 1..534
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="APZ44905R"
 /tissue_type="aboveground organs"
 /dev_stage="two to six-week old"
 /clone_1lb="Arabidopsis thaliana aboveground organs two to
 six-week old"
 /note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
 XhoI"

ORIGIN
 Query Match 82.5%; Score 19.8; DB 9; Length 534;
 Best Local Similarity 91.3%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCCACCAAGAGAGACCCAGAT 24
 |||||
 Db 229 AACCCACCAAGAGAGACCCAGAT 207

RESULT 6
 CK317567/c 705 bp mRNA linear EST 16-DEC-2003
 LOCUS CK317567 Vitis riparia endodermant bud - VRJ Vitis riparia CDNA clone
 DEFINITION VRJ376.3', mRNA sequence.
 ACCESSION CK317567
 VERSION CK317567.1 GI:39952381
 KEYWORDS EST.
 SOURCE Vitis riparia
 ORGANISM Vitis riparia
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; Vitaceae; Vitis.
 1 (bases 1 to 705)
 Fennell, A. and Mathiason, K.
 Expressed sequence tags from endodermant Vitis riparia buds
 Unpublished (2003)
 COMMENT Contact: Anne Fennell
 Horticulture, Forestry, Landscape and Parks Department
 South Dakota State University
 Northern Plains Biostress Laboratory, Box 2140A, Brookings, SD
 57007-0996, USA
 Tel: 605 688 6373

ORIGIN
 Query Match 82.5%; Score 19.8; DB 9; Length 534;
 Best Local Similarity 91.3%; Pred. No. 7.3e+02;
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCCACCAAGAGAGACCCAGAT 24
 |||||
 Db 229 AACCCACCAAGAGAGACCCAGAT 207

Fax: 605 688 4713
Email: Anne.Fennell@edstate.edu
Seq primer: polyT.
Location/Qualifiers

FEATURES

source

1..705
/organism="Vitis riparia"
/mol_type="rRNA"
/db_xref="taxon:96939"
/clone="VRJ376"
/dev_stage="dormant"
/lab_host="DH10B"
/clone_lib="Vitis riparia endodormant bud - VRJ"
/note="Organ: bud; Vector: pSPORT 1; Site 1: SalI; Site 2: NotI; VRJ is a cDNA library of Vitis riparia endodormant buds. Endodormant buds were collected from insect and disease free vines that were induced into dormancy with short photoperiods. The directionally oriented library was constructed according to Gibco BRL Superscript Plasmid System for cDNA synthesis and plasmid cloning."

ORIGIN

Query Match 82.5%; Score 19.8; DB 14; Length 705;
Best Local Similarity 91.3%; Pred. No. 7.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCCACCAAGAGAGACCCGAAAT 24
|||||
Db 297 AGCCACCAAGAGAGACCCGAACT 275

RESULT 7
LOCUS BG024130 1076 bp mRNA linear EST 24-JAN-2001
DEFINITION 602303003F1 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:4394473 5',
mRNA sequence.
ACCESSION BG024130
VERSION BG024130.1 GI:12409388
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1076)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LILAM10090 row: e column: 02
High quality sequence stop: 610.
Location/Qualifiers

1..1076
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4394473"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site 1: NotI; Site 2: SalI; Cloned unidirectionally;
oligo-dt primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: This is a NIH_MGC Library."

FEATURES

source

ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 1076;
Best Local Similarity 91.3%; Pred. No. 8.9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CAGCCACCAAGAGAGACCCGAA 23
|||||
Db 905 CAGCCACCAAGAGAGAGACCCGAA 927

RESULT 8
LOCUS BE729686 1082 bp mRNA linear EST 15-SEP-2000
DEFINITION 60156283F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3832425 5',
mRNA sequence.
ACCESSION BE729686
VERSION BE729686.1 GI:10143678
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1082)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: image.llnl.gov
Plate: LILCM509 row: j column: 10
High quality sequence stop: 737.
Location/Qualifiers

1..1082
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3832425"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 20"
/note="Organ: skin; Vector: pONB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into BcORI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

1..1082
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3832425"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 20"
/note="Organ: skin; Vector: pONB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into BcORI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 82.5%; Score 19.8; DB 10; Length 1082;
Best Local Similarity 91.3%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGCCACCAAGAGAGACCCGAAAT 24
|||||
Db 834 AGCCACCAAGAGAGAGACCCGAAAT 856

RESULT 9
LOCUS AV271379 242 bp mRNA linear EST 05-NOV-1999
DEFINITION AV271379 RIKEN full-length enriched, adult male testis (DH10B) Mus
musculus cDNA clone 4931408J02 3', mRNA sequence.
ACCESSION AV271379
VERSION AV271379.1 GI:6259416
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 242)

Kono,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,M., Sano,M., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Takahashi,F., Tateo,M., Tomimaga,N., Tsunoda,Y., Watanahki,A., Watanabe,S., Yamamura,T., Yasunishi,A., Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Kono,H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki
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Email: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watanahki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

source

location/Qualifiers

1..242

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="493140802"

/sex="male"

/tissue_type="testis"

/dev_stage="adult"

/lab_host="DH10B"

/clone_1lb="RIKEN full-length enriched, adult male testis (DH10B)"

/note="Site_1: SalI, Site_2: BamHI, cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAGATCCAGAGCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGATCTCGATTATTAATTAATCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLCl. Cloning sites, 5' end: SalI, 3' end: BamHI."

ORIGIN

Query Match 80.0%; Score 19.2; DB 9; Length 242;
Best Local Similarity 87.5%; Pred. NO. 1e+03; 3; Indels 0; Gaps 0;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACCCAGAT 24
Db 38 CAGCTATCAAGAGAGACCCAGATT 61

RESULT 10
LOCUS AV333896
DEFINITION AV333896 RIKEN full-length enriched, adult male medulla oblongata
Mus musculus cDNA clone 6330552C10 3', mRNA sequence.
ACCESSION AV333896
VERSION AV333896.1 GI:6373948
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORSTITLE
JOURNAL
COMMENT

Unpublished (1999)

Contact: Yoshihide Hayashizaki
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Fax: 81-45-503-9216

Email: genome-resgsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watanahki,M., Ozawa,K., Tanaka,T., Yoneda,Y., Matsura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)

Itoh,M., Kitsuina,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

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FEATURES

source

location/Qualifiers

1..257

/organism="Mus musculus"

/mol_type="mRNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="6330552C10"

/sex="male"

/tissue_type="medulla oblongata"

/dev_stage="adult"

/lab_host="DH10B"

/clone_1lb="RIKEN full-length enriched, adult male medulla oblongata"

/note="Site_1: SalI, Site_2: BamHI, cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken

ORIGIN

adaported vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

Query Match 80.0%; Score 19.2; DB 28; Length 728;
Best Local Similarity 87.5%; Pred. No. 1.4e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACCCAGAT 24
58 CAGACACCAATATGACCCAGAT 35

RESULT 13

CC518089 899 bp DNA linear GSS 17-JUN-2003
LOCUS CH240_364J21.T7 CHORI-240 Bos taurus genomic clone CH240_364J21,
DEFINITION genomic survey sequence.

ACCESSION CC518089
VERSION CC518089.1 GI:31836377
KEYWORDS GSS.

SOURCE Bos taurus (cow)
ORGANISM Bos taurus

REFERENCE

AUTHORS

Holt, R., Scott, J., Yang, G., Barber, S., Small, D., Prabh, A., L., Tsai, M., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M., Chiu, R., Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S., Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W., Dalmonte, B. P. and Teillac, R.
Bovine BAC End Sequences from Library CHORI-240, PLATTS 294 to 398
Unpublished (2003)
Other GSSs: CH240_364J21.TARBA13P2
Contact: Rob Holt

TITLE

JOURNAL

COMMENT

Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bccsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Place: 364 row: J column: 21
Seq primer: T7
Class: BAC ends.

FEATURES

source

Location/Qualifiers
1..899
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Bred: Hereford"
/db_xref="taxon:9913"
/clone="CH240_364J21"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: PTARAC1.3; Site 1: Mbol; Site 2: Mbol;
Hereford bull LI Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN

Query Match 80.0%; Score 19.2; DB 29; Length 899;
Best Local Similarity 87.5%; Pred. No. 1.5e+03;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACCCAGAT 24
598 CAGCCACCAATATGACCCAGAT 621

RESULT 14

BF901013/c 359 bp mRNA linear EST 18-JAN-2001
LOCUS PM1-MT0203-081200-003-b03 MT0203 Homo sapiens cDNA, mRNA sequence.

DEFINITION BF901013
VERSION BF901013.1 GI:12292472
KEYWORDS EST.

SOURCE

ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R., Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F., Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H., Brunstein, A., deoliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=PM1&t2=PM1-MT0203-
081200-003-b03&t3=2000-12-08&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 359.

FEATURES

source

Location/Qualifiers
1..359
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="MT0203"
/note="Organ: marrow; Vector: puc18; Site 1: SmaI; Site 2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

ORIGIN

Query Match 79.2%; Score 19; DB 10; Length 359;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CAGCCACCAAGAGAGACCC 19
137 CAGCCACCAAGAGAGACCC 119

RESULT 15

CD557470/c 897 bp mRNA linear EST 11-JUN-2003
LOCUS CD557470
DEFINITION AGENCOURT_14413595 NIH_MGC_180 Homo sapiens cDNA clone

